



SEQUENCE LISTING

<110> Sheppard, Paul O.

<120> IL-28 AND IL-29 TRUNCATED CYSTEINE
MUTANTS AND METHODS OF USING SAME

<130> 05-22P1

<160> 150

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 618

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(618)

<221> misc_feature

<222> (0)...(0)

<223> IL-28A

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acc gtg act gga gca gtt cct gtc gcc agg ctc cac ggg gct ctc ccg 96
Thr Val Thr Gly Ala Val Pro Val Ala Arg Leu His Gly Ala Leu Pro 30
20 25
gat gca agg ggc tgc cac ata gcc cag ttc aag tcc ctg tct cca cag 144
Asp Ala Arg Gly Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln 45
35 40
gag ctg cag gcc ttt aag agg gcc aaa gat gcc tta gaa gag tgc ctt 192
Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu 60
50 55
ctg ctg aag gac tgc agg tgc cac tcc cgc ctc ttc ccc agg acc tgg 240
Leu Leu Lys Asp Cys Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp 80
65 70 75
gac ctg agg cag ctg cag gtg agg gag cgc ccc atg gct ttg gag gct 288
Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala 95
85
gag ctg gcc ctg acg ctg aag gtt ctg gag gcc acc gct gac act gac 336
Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp 110
100 105
cca gcc ctg gtg gac gtc ttg gac cag ccc ctt cac acc ctg cac cat 384
Pro Ala Leu Val Asp Val Leu Asp Gln Pro Leu His Thr Leu His His 125
115
atc ctc tcc cag ttc cgg gcc tgt gtg agt cgt cag ggc ctg ggc acc 432
Ile Leu Ser Gln Phe Arg Ala Cys Val Ser Arg Gln Gly Leu Gly Thr 140
130 135
cag atc cag cct cag ccc acg gca ggg ccc agg acc cgg ggc cgc ctc 480

Gln Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly Arg Leu
 145 150 155 160
 cac cat tgg ctg tac cgg ctc cag gag gcc cca aaa aag gag tcc cct 528
 His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Pro
 165 170 175
 ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc ctc ctc acg 576
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 180 185 190
 cga gac ctg aat tgt gtt gcc agt ggg gac ctg tgt gtc tga 618
 Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val *
 195 200 205

<210> 2
 <211> 205
 <212> PRT
 <213> Homo sapiens

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 20 25 30
 Asp Ala Arg Gly Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln
 35 40 45
 Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu
 50 55 60
 Leu Leu Lys Asp Cys Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp
 65 70 75 80
 Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala
 85 90 95
 Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp
 100 105 110
 Pro Ala Leu Val Asp Val Leu Asp Gln Pro Leu His Thr Leu His His
 115 120 125
 Ile Leu Ser Gln Phe Arg Ala Cys Val Ser Arg Gln Gly Leu Gly Thr
 130 135 140
 Gln Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly Arg Leu
 145 150 155 160
 His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Pro
 165 170 175
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 180 185 190
 Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 195 200 205

<210> 3
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (1)...(603)
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 <223> IL-29

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gcc gtg gca ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag 96
 Ala Val Ala Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys 30
 20 25

ggc tgc cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg 144
 Gly Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala 45
 35 40

agc ttc aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa 192
 Ser Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys 60
 50 55

aac tgg agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg 240
 Asn Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg 80
 65 70 75

ctt ctc cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc 288
 Leu Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala 95
 85 90

ctg acg ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac 336
 Leu Thr Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp 110
 100 105

gtc cta gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc 384
 Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu 125
 115 120

cag gcc tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg gcc 432
 Gln Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly 140
 130 135

cgc ctc cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag 480
 Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu 160
 145 150 155

tcc gct ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc 528
 Ser Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu 175
 165 170

ctc acg cga gac ctc aaa tat gtg gcc gat ggg gac ctg tgt ctg aga 576
 Leu Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg 190
 180 185

acg tca acc cac cct gag tcc acc tga 603
 Thr Ser Thr His Pro Glu Ser Thr *
 195 200

<210> 4
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 <212> PRT
 <213> Homo sapiens

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 Gly Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala 45
 35 40

Ser Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys
 50 55 60
 Asn Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg
 65 70 75 80
 Leu Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala
 85 90 95
 Leu Thr Leu Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp
 100 105 110
 Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu
 115 120 125
 Gln Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly
 130 135 140
 Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu
 145 150 155 160
 Ser Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
 165 170 175
 Leu Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg
 180 185 190
 Thr Ser Thr His Pro Glu Ser Thr
 195 200

<210> 5
 <211> 615
 <212> DNA
 <213> Homo sapiens

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 acc gtg act gga gca gtt cct gtc gcc agg ctc cgc ggg gct ctc ccg 96
 Thr Val Thr Gly Ala Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro 30
 20 25
 gat gca agg ggc tgc cac ata gcc cag ttc aag tcc ctg tct cca cag 144
 Asp Ala Arg Gly Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln 45
 35 40
 gag ctg cag gcc ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt 192
 Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu 60
 50 55
 ctg ctg aag gac tgc aag tgc cgc tcc cgc ctc ttc ccc agg acc tgg 240
 Leu Leu Lys Asp Cys Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp 80
 65 70 75
 gac ctg agg cag ctg cag gtg agg gag cgc ccc gtg gct ttg gag gct 288
 Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala 95
 85 90
 gag ctg gcc ctg acg ctg aag gtt ctg gag gcc acc gct gac act gac 336
 Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp 110
 100 105
 cca gcc ctg ggg gat gtc ttg gac cag ccc ctt cac acc ctg cac cat 384

Pro Ala Leu Gly Asp Val Leu Asp Gln Pro Leu His Thr Leu His His
 115 120 125

atc ctc tcc cag ctc cgg gcc tgt gtg agt cgt cag ggc ccg ggc acc 432
 Ile Leu Ser Gln Leu Arg Ala Cys Val Ser Arg Gln Gly Pro Gly Thr
 130 135 140

cag atc cag cct cag ccc acg gca ggg ccc agg acc cgg ggc cgc ctc 480
 Gln Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly Arg Leu
 145 150 155 160

cac cat tgg ctg cac cgg ctc cag gag gcc cca aaa aag gag tcc cct 528
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Pro
 165 170 175

ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc ctc ctc acg 576
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 180 185 190

cgā gac ctg aat tgt gtt gcc agc ggg gac ctg tgt gtc 615
 Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 195 200 205

<210> 6
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 <212> PRT
 <213> Homo sapiens

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 Asp Ala Arg Gly Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln
 35 40 45
 Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu
 50 55 60
 Leu Leu Lys Asp Cys Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp
 65 70 75 80
 Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala
 85 90 95
 Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp
 100 105 110
 Pro Ala Leu Gly Asp Val Leu Asp Gln Pro Leu His Thr Leu His His
 115 120 125
 Ile Leu Ser Gln Leu Arg Ala Cys Val Ser Arg Gln Gly Pro Gly Thr
 130 135 140
 Gln Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly Arg Leu
 145 150 155 160
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Pro
 165 170 175
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 180 185 190
 Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 195 200 205

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<220>
 <221> CDS

<222> (22)...(630)

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Leu Leu Leu Leu Leu Pro Leu Leu Leu Ala Ala Val Leu Thr Arg Thr		
	15 20 25	
caa gct gac cct gtc ccc agg gcc acc agg ctc cca gtg gaa gca aag	147	
Gln Ala Asp Pro Val Pro Arg Ala Thr Arg Leu Pro Val Glu Ala Lys		
	30 35 40	
gat tgc cac att gct cag ttc aag tct ctg tcc cca aaa gag ctg cag	195	
Asp Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Lys Glu Leu Gln		
	45 50 55	
gcc ttc aaa aag gcc aag gat gcc atc gag aag agg ctg ctt gag aag	243	
Ala Phe Lys Lys Ala Lys Asp Ala Ile Glu Lys Arg Leu Leu Glu Lys		
	60 65 70	
gac ctg agg tgc agt tcc cac ctc ttc ccc agg gcc tgg gac ctg aag	291	
Asp Leu Arg Cys Ser Ser His Leu Phe Pro Arg Ala Trp Asp Leu Lys		
	75 80 85 90	
cag ctg cag gtc caa gag cgc ccc aag gcc ttg cag gct gag gtg gcc	339	
Gln Leu Gln Val Gln Glu Arg Pro Lys Ala Leu Gln Ala Glu Val Ala		
	95 100 105	
ctg acc ctg aag gtc tgg gag aac atg act gac tca gcc ctg gcc acc	387	
Leu Thr Leu Lys Val Trp Glu Asn Met Thr Asp Ser Ala Leu Ala Thr		
	110 115 120	
atc ctg ggc cag cct ctt cat aca ctg agc cac att cac tcc cag ctg	435	
Ile Leu Gly Gln Pro Leu His Thr Leu Ser His Ile His Ser Gln Leu		
	125 130 135	
cag acc tgt aca cag ctt cag gcc aca gca gag ccc agg tcc ccg agc	483	
Gln Thr Cys Thr Gln Leu Gln Ala Thr Ala Glu Pro Arg Ser Pro Ser		
	140 145 150	
cgc cgc ctc tcc cgc tgg ctg cac agg ctc cag gag gcc cag agc aag	531	
Arg Arg Leu Ser Arg Trp Leu His Arg Leu Gln Glu Ala Gln Ser Lys		
	155 160 165 170	
gag acc cct ggc tgc ctg gag gcc tct gtc acc tcc aac ctg ttt cgc	579	
Glu Thr Pro Gly Cys Leu Glu Ala Ser Val Thr Ser Asn Leu Phe Arg		
	175 180 185	
ctg ctc acc cgg gac ctc aag tgt gtg gcc aat gga gac cag tgt gtc	627	
Leu Leu Thr Arg Asp Leu Lys Cys Val Ala Asn Gly Asp Gln Cys Val		
	190 195 200	
tga cct	633	
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<210> 8

<211> 202

<212> PRT

<213> Mus musculus

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 Arg Ala Thr Arg Leu Pro Val Glu Ala Lys Asp Cys His Ile Ala Gln
 35 40 45
 Phe Lys Ser Leu Ser Pro Lys Glu Leu Gln Ala Phe Lys Lys Ala Lys
 50 55 60
 Asp Ala Ile Glu Lys Arg Leu Leu Glu Lys Asp Leu Arg Cys Ser Ser
 65 70 75 80
 His Leu Phe Pro Arg Ala Trp Asp Leu Lys Gln Leu Gln Val Gln Glu
 85 90 95
 Arg Pro Lys Ala Leu Gln Ala Glu Val Ala Leu Thr Leu Lys Val Trp
 100 105 110
 Glu Asn Met Thr Asp Ser Ala Leu Ala Thr Ile Leu Gly Gln Pro Leu
 115 120 125
 His Thr Leu Ser His Ile His Ser Gln Leu Gln Thr Cys Thr Gln Leu
 130 135 140
 Gln Ala Thr Ala Glu Pro Arg Ser Pro Ser Arg Arg Leu Ser Arg Trp
 145 150 155 160
 Leu His Arg Leu Gln Glu Ala Gln Ser Lys Glu Thr Pro Gly Cys Leu
 165 170 175
 Glu Ala Ser Val Thr Ser Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu
 180 185 190
 Lys Cys Val Ala Asn Gly Asp Gln Cys Val
 195 200

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 <212> DNA
 <213> Mus musculus

<220>
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 <222> (22) ... (630)

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 Leu Leu Leu Leu Leu Pro Leu Leu Leu Ala Ala Val Leu Thr Arg Thr 25
 15 20
 caa gct gac cct gtc ccc agg gcc acc agg ctc cca gtg gaa gca aag 147
 Gln Ala Asp Pro Val Pro Arg Ala Thr Arg Leu Pro Val Glu Ala Lys 40
 30 35
 gat tgc cac att gct cag ttc aag tct ctg tcc cca aaa gag ctg cag 195
 Asp Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Lys Glu Leu Gln 55
 45 50
 gcc ttc aaa aag gcc aag ggt gcc atc gag aag agg ctg ctt gag aag 243
 Ala Phe Lys Lys Ala Lys Gly Ala Ile Glu Lys Arg Leu Leu Glu Lys 70
 60 65
 gac atg agg tgc agt tcc cac ctc atc tcc agg gcc tgg gac ctg aag 291
 Asp Met Arg Cys Ser Ser His Leu Ile Ser Arg Ala Trp Asp Leu Lys 90
 75 80 85
 cag ctg cag gtc caa gag cgc ccc aag gcc ttg cag gct gag gtg gcc 339
 Gln Leu Gln Val Gln Glu Arg Pro Lys Ala Leu Gln Ala Glu Val Ala

95 100 105
 ctg acc ctg aag gtc tgg gag aac ata aat gac tca gcc ctg acc acc 387
 Leu Thr Leu Lys Val Trp Glu Asn Ile Asn Asp Ser Ala Leu Thr Thr
 110 115 120
 atc ctg ggc cag cct ctt cat aca ctg agc cac att cac tcc cag ctg 435
 Ile Leu Gly Gln Pro Leu His Thr Leu Ser His Ile His Ser Gln Leu
 125 130 135
 cag acc tgt aca cag ctt cag gcc aca gca gag ccc aag ccc ccg agt 483
 Gln Thr Cys Thr Gln Leu Gln Ala Thr Ala Glu Pro Lys Pro Pro Ser
 140 145 150
 cgc cgc ctc tcc cgc tgg ctg cac agg ctc cag gag gcc cag agc aag 531
 Arg Arg Leu Ser Arg Trp Leu His Arg Leu Gln Glu Ala Gln Ser Lys
 155 160 165 170
 gag act cct ggc tgc ctg gag gac tct gtc acc tcc aac ctg ttt caa 579
 Glu Thr Pro-Gly-Cys-Leu Glu Asp Ser Val Thr Ser Asn Leu Phe Gln
 175 180 185
 ctg ctc ctc cgg gac ctc aag tgt gtg gcc agt gga gac cag tgt gtc 627
 Leu Leu Leu Arg Asp Leu Lys Cys Val Ala Ser Gly Asp Gln Cys Val
 190 195 200
 tga cc 632
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<210> 10
 <211> 202
 <212> PRT
 <213> Mus musculus

<400> 10
 Met Lys Pro Glu Thr Ala Gly Gly His Met Leu Leu Leu Leu Leu Pro
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 20 25 30
 Arg Ala Thr Arg Leu Pro Val Glu Ala Lys Asp Cys His Ile Ala Gln
 35 40 45
 Phe Lys Ser Leu Ser Pro Lys Glu Leu Gln Ala Phe Lys Lys Ala Lys
 50 55 60
 Gly Ala Ile Glu Lys Arg Leu Leu Glu Lys Asp Met Arg Cys Ser Ser
 65 70 75 80
 His Leu Ile Ser Arg Ala Trp Asp Leu Lys Gln Leu Gln Val Gln Glu
 85 90 95
 Arg Pro Lys Ala Leu Gln Ala Glu Val Ala Leu Thr Leu Lys Val Trp
 100 105 110
 Glu Asn Ile Asn Asp Ser Ala Leu Thr Thr Ile Leu Gly Gln Pro Leu
 115 120 125
 His Thr Leu Ser His Ile His Ser Gln Leu Gln Thr Cys Thr Gln Leu
 130 135 140
 Gln Ala Thr Ala Glu Pro Lys Pro Pro Ser Arg Arg Leu Ser Arg Trp
 145 150 155 160
 Leu His Arg Leu Gln Glu Ala Gln Ser Lys Glu Thr Pro Gly Cys Leu
 165 170 175
 Glu Asp Ser Val Thr Ser Asn Leu Phe Gln Leu Leu Leu Arg Asp Leu
 180 185 190
 Lys Cys Val Ala Ser Gly Asp Gln Cys Val 200
 195

<210> 11
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 <212> DNA
 <213> Homo sapiens

<220>
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 <223> IL-28RA

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 gcc gct cca ggg agg ccc cgt ctg gcc cct ccc cag aat gtg acg ctg 96
 Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
 20 25 30
 ctc tcc cag aac ttc agc gtg tac ctg aca tgg ctc cca ggg ctt ggc 144
 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly
 35 40 45
 aac ccc cag gat gtg acc tat ttt gtg gcc tat cag agc tct ccc acc 192
 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr
 50 55 60
 cgt aga cgg tgg cgc gaa gtg gaa gag tgt gcg gga acc aag gag ctg 240
 Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu
 65 70 75 80
 cta tgt tct atg atg tgc ctg aag aaa cag gac ctg tac aac aag ttc 288
 Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe
 85 90 95
 aag gga cgc gtg cgg acg gtt tct ccc agc tcc aag tcc ccc tgg gtg 336
 Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val
 100 105 110
 gag tcc gaa tac ctg gat tac ctt ttt gaa gtg gag ccg gcc cca cct 384
 Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro
 115 120 125
 gtc ctg gtg ctc acc cag acg gag gag atc ctg agt gcc aat gcc acg 432
 Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr
 130 135 140
 tac cag ctg ccc ccc tgc atg ccc cca ctg gat ctg aag tat gag gtg 480
 Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val
 145 150 155 160
 gca ttc tgg aag gag ggg gcc gga aac aag acc cta ttt cca gtc act 528
 Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Thr Leu Phe Pro Val Thr
 165 170 175
 ccc cat ggc cag cca gtc cag atc act ctc cag cca gct gcc agc gaa 576
 Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu
 180 185 190
 cac cac tgc ctc agt gcc aga acc atc tac acg ttc agt gtc ccg aaa 624
 His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys
 195 200 205

tac agc aag ttc tct aag ccc acc tgc ttc ttg ctg gag gtc cca gaa Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro Glu 210 215 220	672
gcc aac tgg gct ttc ctg gtg ctg cca tcg ctt ctg ata ctg ctg tta Ala Asn Trp Ala Phe Leu Val Leu Pro Ser Leu Leu Ile Leu Leu Leu 225 230 235 240	720
gta att gcc gca ggg ggt gtg atc tgg aag acc ctc atg ggg aac ccc Val Ile Ala Ala Gly Gly Val Ile Trp Lys Thr Leu Met Gly Asn Pro 245 250 255	768
tgg ttt cag cgg gca aag atg cca cgg gcc ctg gac ttt tct gga cac Trp Phe Gln Arg Ala Lys Met Pro Arg Ala Leu Asp Phe Ser Gly His 260 265 270	816
aca cac cct gtg gca acc ttt cag ccc agc aga cca gag tcc gtg aat Thr His Pro Val Ala Thr Phe Gln Pro Ser Arg Pro Glu Ser Val Asn 275 280 285	864
gac ttg ttc ctc tgt ccc caa aag gaa ctg acc aga ggg gtc agg ccg Asp Leu Phe Leu Cys Pro Gln Lys Glu Leu Thr Arg Gly Val Arg Pro 290 295 300	912
acg cct cga gtc agg gcc cca gcc acc caa cag aca aga tgg aag aag Thr Pro Arg Val Arg Ala Pro Ala Thr Gln Gln Thr Arg Trp Lys Lys 305 310 315 320	960
gac ctt gca gag gac gaa gag gag gag gat gag gag gac aca gaa gat Asp Leu Ala Glu Asp Glu Glu Glu Glu Asp Glu Glu Asp Thr Glu Asp 325 330 335	1008
ggc gtc agc ttc cag ccc tac att gaa cca cct tct ttc ctg ggg caa Gly Val Ser Phe Gln Pro Tyr Ile Glu Pro Pro Ser Phe Leu Gly Gln 340 345 350	1056
gag cac cag gct cca ggg cac tcg gag gct ggt ggg gtg gac tca ggg Glu His Gln Ala Pro Gly His Ser Glu Ala Gly Gly Val Asp Ser Gly 355 360 365	1104
agg ccc agg gct cct ctg gtc cca agc gaa ggc tcc tct gct tgg gat Arg Pro Arg Ala Pro Leu Val Pro Ser Glu Gly Ser Ser Ala Trp Asp 370 375 380	1152
tct tca gac aga agc tgg gcc agc act gtg gac tcc tcc tgg gac agg Ser Ser Asp Arg Ser Trp Ala Ser Thr Val Asp Ser Ser Trp Asp Arg 385 390 395 400	1200
gct ggg tcc tct ggc tat ttg gct gag aag ggg cca ggc caa ggg ccg Ala Gly Ser Ser Gly Tyr Leu Ala Glu Lys Gly Pro Gly Gln Gly Pro 405 410 415	1248
ggt ggg gat ggg cac caa gaa tct ctc cca cca cct gaa ttc tcc aag Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Pro Glu Phe Ser Lys 420 425 430	1296
gac tcg ggt ttc ctg gaa gag ctc cca gaa gat aac ctc tcc tcc tgg Asp Ser Gly Phe Leu Glu Glu Leu Pro Glu Asp Asn Leu Ser Ser Trp 435 440 445	1344
gcc acc tgg ggc acc tta cca ccg gag ccg aat ctg gtc cct ggg gga Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Asn Leu Val Pro Gly Gly 450 455 460	1392

ccc cca gtt tct ctt cag aca ctg acc ttc tgc tgg gaa agc agc cct 1440
 Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu Ser Ser Pro
 465 470 475 480
 gag gag gaa gag gag gcg agg gaa tca gaa att gag gac agc gat gcg 1488
 Glu Glu Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp Ser Asp Ala
 485 490 495
 ggc agc tgg ggg gct gag agc acc cag agg acc gag gac agg ggc cgg 1536
 Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp Arg Gly Arg
 500 505 510
 aca ttg ggg cat tac atg gcc agg tga 1563
 Thr Leu Gly His Tyr Met Ala Arg *
 515 520

<210> 12
 <211> 520
 <212> PRT
 <213> Homo sapiens

<400> 12
 Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln
 1 5 10 15
 Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
 20 25 30
 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly
 35 40 45
 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr
 50 55 60
 Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu
 65 70 75 80
 Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe
 85 90 95
 Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val
 100 105 110
 Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro
 115 120 125
 Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr
 130 135 140
 Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val
 145 150 155 160
 Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Thr Leu Phe Pro Val Thr
 165 170 175
 Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu
 180 185 190
 His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys
 195 200 205
 Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro Glu
 210 215 220
 Ala Asn Trp Ala Phe Leu Val Leu Pro Ser Leu Leu Ile Leu Leu Leu
 225 230 235 240
 Val Ile Ala Ala Gly Gly Val Ile Trp Lys Thr Leu Met Gly Asn Pro
 245 250 255
 Trp Phe Gln Arg Ala Lys Met Pro Arg Ala Leu Asp Phe Ser Gly His
 260 265 270
 Thr His Pro Val Ala Thr Phe Gln Pro Ser Arg Pro Glu Ser Val Asn
 275 280 285
 Asp Leu Phe Leu Cys Pro Gln Lys Glu Leu Thr Arg Gly Val Arg Pro
 290 295 300
 Thr Pro Arg Val Arg Ala Pro Ala Thr Gln Gln Thr Arg Trp Lys Lys
 305 310 315 320
 Asp Leu Ala Glu Asp Glu Glu Glu Glu Asp Glu Glu Asp Thr Glu Asp
 325 330 335

Gly Val Ser Phe Gln Pro Tyr Ile Glu Pro Pro Ser Phe Leu Gly Gln
 340 345 350
 Glu His Gln Ala Pro Gly His Ser Glu Ala Gly Gly Val Asp Ser Gly
 355 360 365
 Arg Pro Arg Ala Pro Leu Val Pro Ser Glu Gly Ser Ser Ala Trp Asp
 370 375 380
 Ser Ser Asp Arg Ser Trp Ala Ser Thr Val Asp Ser Ser Trp Asp Arg
 385 390 395 400
 Ala Gly Ser Ser Gly Tyr Leu Ala Glu Lys Gly Pro Gly Gln Gly Pro
 405 410 415
 Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Pro Glu Phe Ser Lys
 420 425 430
 Asp Ser Gly Phe Leu Glu Glu Leu Pro Glu Asp Asn Leu Ser Ser Trp
 435 440 445
 Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Asn Leu Val Pro Gly Gly
 450 455 460
 Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu Ser Ser Pro
 465 470 475 480
 Glu Glu Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp Ser Asp Ala
 485 490 495
 Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp Arg Gly Arg
 500 505 510
 Thr Leu Gly His Tyr Met Ala Arg
 515 520

<210> 13
 <211> 1476
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1476)

<221> misc_feature
 <222> (0)...(0)
 <223> IL-28RA splice variant

<400> 13
 atg gcg ggg ccc gag cgc tgg ggc ccc ctg ctc ctg tgc ctg ctg cag 48
 Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln
 1 5 10 15
 gcc gct cca ggg agg ccc cgt ctg gcc cct ccc cag aat gtg acg ctg 96
 Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
 20 25 30
 ctc tcc cag aac ttc agc gtg tac ctg aca tgg ctc cca ggg ctt ggc 144
 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly
 35 40 45
 aac ccc cag gat gtg acc tat ttt gtg gcc tat cag agc tct ccc acc 192
 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr
 50 55 60
 cgt aga cgg tgg cgc gaa gtg gaa gag tgt gcg gga acc aag gag ctg 240
 Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu
 65 70 75 80
 cta tgt tct atg atg tgc ctg aag aaa cag gac ctg tac aac aag ttc 288
 Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe
 85 90 95
 aag gga cgc gtg cgg acg gtt tct ccc agc tcc aag tcc ccc tgg gtg 336

Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val	100	105	110	
gag tcc gaa tac ctg gat tac ctt ttt gaa gtg gag ccg gcc cca cct	115	120	125	384
Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro				
gtc ctg gtg ctc acc cag acg gag gag atc ctg agt gcc aat gcc acg	130	135	140	432
Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr				
tac cag ctg ccc ccc tgc atg ccc cca ctg ttt ctg aag tat gag gtg	145	150	155	480
Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Phe Leu Lys Tyr Glu Val				
gca ttt tgg ggg ggg ggg gcc gga acc aag acc cta ttt cca gtc act	165	170	175	528
Ala Phe Trp Gly Gly Gly Ala Gly Thr Lys Thr Leu Phe Pro Val Thr				
ccc cat ggc cag cca gtc cag atc act ctc cag cca gct gcc agc gaa	180	185	190	576
Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu				
cac cac tgc ctc agt gcc aga acc atc tac acg ttc agt gtc ccg aaa	195	200	205	624
His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys				
tac agc aag ttc tct aag ccc acc tgc ttc ttg ctg gag gtc cca gaa	210	215	220	672
Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro Glu				
gcc aac tgg gct ttc ctg gtg ctg cca tcg ctt ctg ata ctg ctg tta	225	230	235	720
Ala Asn Trp Ala Phe Leu Val Leu Pro Ser Leu Leu Ile Leu Leu Leu				
gta att gcc gca ggg ggt gtg atc tgg aag acc ctc atg ggg aac ccc	245	250	255	768
Val Ile Ala Ala Gly Gly Val Ile Trp Lys Thr Leu Met Gly Asn Pro				
tgg ttt cag cgg gca aag atg cca cgg gcc ctg gaa ctg acc aga ggg	260	265	270	816
Trp Phe Gln Arg Ala Lys Met Pro Arg Ala Leu Glu Leu Thr Arg Gly				
gtc agg ccg acg cct cga gtc agg gcc cca gcc acc caa cag aca aga	275	280	285	864
Val Arg Pro Thr Pro Arg Val Arg Ala Pro Ala Thr Gln Gln Thr Arg				
tgg aag aag gac ctt gca gag gac gaa gag gag gag gat gag gag gac	290	295	300	912
Trp Lys Lys Asp Leu Ala Glu Asp Glu Glu Glu Asp Glu Glu Asp				
aca gaa gat ggc gtc agc ttc cag ccc tac att gaa cca cct tct ttc	305	310	315	960
Thr Glu Asp Gly Val Ser Phe Gln Pro Tyr Ile Glu Pro Pro Ser Phe				
ctg ggg caa gag cac cag gct cca ggg cac tcg gag gct ggt ggg gtg	325	330	335	1008
Leu Gly Gln Glu His Gln Ala Pro Gly His Ser Glu Ala Gly Gly Val				
gac tca ggg agg ccc agg gct cct ctg gtc cca agc gaa ggc tcc tct	340	345	350	1056
Asp Ser Gly Arg Pro Arg Ala Pro Leu Val Pro Ser Glu Gly Ser Ser				
gct tgg gat tct tca gac aga agc tgg gcc agc act gtg gac tcc tcc				1104
Ala Trp Asp Ser Ser Asp Arg Ser Trp Ala Ser Thr Val Asp Ser Ser				

355 360 365

1152
 tgg gac agg gct ggg tcc tct ggc tat ttg gct gag aag ggg cca ggc
 Trp Asp Arg Ala Gly Ser Ser Gly Tyr Leu Ala Glu Lys Gly Pro Gly
 370 375 380

1200
 caa ggg ccg ggt ggg gat ggg cac caa gaa tct ctc cca cca cct gaa
 Gln Gly Pro Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Pro Glu
 385 390 395 400

1248
 ttc tcc aag gac tcg ggt ttc ctg gaa gag ctc cca gaa gat aac ctc
 Phe Ser Lys Asp Ser Gly Phe Leu Glu Glu Leu Pro Glu Asp Asn Leu
 405 410 415

1296
 tcc tcc tgg gcc acc tgg ggc acc tta cca ccg gag ccg aat ctg gtc
 Ser Ser Trp Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Asn Leu Val
 420 425 430

1344
 cct ggg gga ccc cca gtt tct ctt cag aca ctg acc ttc tgc tgg gaa
 Pro Gly Gly Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu
 435 440 445

1392
 agc agc cct gag gag gaa gag gag gcg agg gaa tca gaa att gag gac
 Ser Ser Pro Glu Glu Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp
 450 455 460

1440
 agc gat gcg ggc agc tgg ggg gct gag agc acc cag agg acc gag gac
 Ser Asp Ala Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp
 465 470 475 480

1476
 agg ggc cgg aca ttg ggg cat tac atg gcc agg tga
 Arg Gly Arg Thr Leu Gly His Tyr Met Ala Arg *
 485 490

<210> 14
 <211> 491
 <212> PRT
 <213> Homo sapiens

<400> 14
 Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln
 1 5 10 15
 Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
 20 25 30
 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly
 35 40 45
 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr
 50 55 60
 Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu
 65 70 75 80
 Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe
 85 90 95
 Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val
 100 105 110
 Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro
 115 120 125
 Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr
 130 135 140
 Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Phe Leu Lys Tyr Glu Val
 145 150 155 160
 Ala Phe Trp Gly Gly Ala Gly Thr Lys Thr Leu Phe Pro Val Thr
 165 170 175
 Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu
 180 185 190

His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys
 195 200 205
 Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro Glu
 210 215 220
 Ala Asn Trp Ala Phe Leu Val Leu Pro Ser Leu Leu Ile Leu Leu Leu
 225 230 235 240
 Val Ile Ala Ala Gly Gly Val Ile Trp Lys Thr Leu Met Gly Asn Pro
 245 250 255
 Trp Phe Gln Arg Ala Lys Met Pro Arg Ala Leu Glu Leu Thr Arg Gly
 260 265 270
 Val Arg Pro Thr Pro Arg Val Arg Ala Pro Ala Thr Gln Gln Thr Arg
 275 280 285
 Trp Lys Lys Asp Leu Ala Glu Asp Glu Glu Glu Glu Asp Glu Glu Asp
 290 295 300
 Thr Glu Asp Gly Val Ser Phe Gln Pro Tyr Ile Glu Pro Pro Ser Phe
 305 310 315 320
 Leu Gly Gln Glu His Gln Ala Pro Gly His Ser Glu Ala Gly Gly Val
 325 330 335
 Asp Ser Gly Arg Pro Arg Ala Pro Leu Val Pro Ser Glu Gly Ser Ser
 340 345 350
 Ala Trp Asp Ser Ser Asp Arg Ser Trp Ala Ser Thr Val Asp Ser Ser
 355 360 365
 Trp Asp Arg Ala Gly Ser Ser Gly Tyr Leu Ala Glu Lys Gly Pro Gly
 370 375 380
 Gln Gly Pro Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Pro Glu
 385 390 395 400
 Phe Ser Lys Asp Ser Gly Phe Leu Glu Glu Leu Pro Glu Asp Asn Leu
 405 410 415
 Ser Ser Trp Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Asn Leu Val
 420 425 430
 Pro Gly Gly Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu
 435 440 445
 Ser Ser Pro Glu Glu Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp
 450 455 460
 Ser Asp Ala Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp
 465 470 475 480
 Arg Gly Arg Thr Leu Gly His Tyr Met Ala Arg
 485 490

<210> 15
 <211> 674
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(636)

<221> misc_feature
 <222> (0)...(0)
 <223> IL-28RA soluble variant

<400> 15
 atg gcg ggg ccc gag cgc tgg ggc ccc ctg ctc ctg tgc ctg ctg cag 48
 Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln
 1 5 10 15
 gcc gct cca ggg agg ccc cgt ctg gcc cct ccc cag aat gtg acg ctg 96
 Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
 20 25 30
 ctc tcc cag aac ttc agc gtg tac ctg aca tgg ctc cca ggg ctt ggc 144
 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly
 35 40 45

aac ccc cag gat gtg acc tat ttt gtg gcc tat cag agc tct ccc acc 192
 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr
 50 55 60

cgt aga cgg tgg cgc gaa gtg gaa gag tgt gcg gga acc aag gag ctg 240
 Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu
 65 70 75 80

cta tgt tct atg atg tgc ctg aag aaa cag gac ctg tac aac aag ttc 288
 Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe
 85 90 95

aag gga cgc gtg cgg acg gtt tct ccc agc tcc aag tcc ccc tgg gtg 336
 Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val
 100 105 110

gag tcc gaa tac ctg gat tac ctt ttt gaa gtg gag ccg gcc cca cct 384
 Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro
 115 120 125

gtc ctg gtg ctc acc cag acg gag gag atc ctg agt gcc aat gcc acg 432
 Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr
 130 135 140

tac cag ctg ccc ccc tgc atg ccc cca ctg gat ctg aag tat gag gtg 480
 Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val
 145 150 155 160

gca ttc tgg aag gag ggg gcc gga aac aag gtg gga agc tcc ttt cct 528
 Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Val Gly Ser Ser Phe Pro
 165 170 175

gcc ccc agg cta ggc ccg ctc ctc cac ccc ttc tta ctc agg ttc ttc 576
 Ala Pro Arg Leu Gly Pro Leu Leu His Pro Phe Leu Leu Arg Phe Phe
 180 185 190

tca ccc tcc cag cct gct cct gca ccc ctc ctc cag gaa gtc ttc cct 624
 Ser Pro Ser Gln Pro Ala Pro Ala Pro Leu Leu Gln Glu Val Phe Pro
 195 200 205

gta cac tcc tga cttctggcag tcagccctaa taaaatctga tcaaagta 674
 Val His Ser *
 210

<210> 16
 <211> 211
 <212> PRT
 <213> Homo sapiens

<400> 16
 Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln
 1 5 10 15
 Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
 20 25 30
 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly
 35 40 45
 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr
 50 55 60
 Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu
 65 70 75 80
 Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe
 85 90 95
 Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val

100 105 110
 Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro
 115 120 125
 Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr
 130 135 140
 Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val
 145 150 155 160
 Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Val Gly Ser Ser Phe Pro
 165 170 175
 Ala Pro Arg Leu Gly Pro Leu Leu His Pro Phe Leu Leu Arg Phe Phe
 180 185 190
 Ser Pro Ser Gln Pro Ala Pro Ala Pro Leu Leu Gln Glu Val Phe Pro
 195 200 205
 Val His Ser
 210

<210> 17
 <211> 734
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> (53)...(127)
 <221> mat_peptide
 <222> (128)...(655)

<221> CDS
 <222> (53)...(655)

<400> 17
 tgggtgacag cctcagagtg tttcttctgc tgacaaagac cagagatcag ga atg aaa 58
 Met Lys
 -25

cta gac atg act ggg gac tgc acg cca gtg ctg gtg ctg atg gcc gca 106
 Leu Asp Met Thr Gly Asp Cys Thr Pro Val Leu Val Leu Met Ala Ala
 -20 -15 -10

gtg ctg acc gtg act gga gca gtt cct gtc gcc agg ctc cac ggg gct 154
 Val Leu Thr Val Thr Gly Ala Val Pro Val Ala Arg Leu His Gly Ala
 -5 1 5

ctc ccg gat gca agg ggc tgc cac ata gcc cag ttc aag tcc ctg tct 202
 Leu Pro Asp Ala Arg Gly Cys His Ile Ala Gln Phe Lys Ser Leu Ser
 10 15 20 25

cca cag gag ctg cag gcc ttt aag agg gcc aaa gat gcc tta gaa gag 250
 Pro Gln Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu
 30 35 40

tcg ctt ctg ctg aag gac tgc agg tgc cac tcc cgc ctc ttc ccc agg 298
 Ser Leu Leu Leu Lys Asp Cys Arg Cys His Ser Arg Leu Phe Pro Arg
 45 50 55

acc tgg gac ctg agg cag ctg cag gtg agg gag cgc ccc atg gct ttg 346
 Thr Trp Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Met Ala Leu
 60 65 70

gag gct gag ctg gcc ctg acg ctg aag gtt ctg gag gcc acc gct gac 394
 Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr Ala Asp
 75 80 85

act gac cca gcc ctg gtg gac gtc ttg gac cag ccc ctt cac acc ctg 442
 Thr Asp Pro Ala Leu Val Asp Val Leu Asp Gln Pro Leu His Thr Leu 105
 90 95 100
 cac cat atc ctc tcc cag ttc cgg gcc tgt atc cag cct cag ccc acg 490
 His His Ile Leu Ser Gln Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr 120
 110 115
 gca ggg ccc agg acc cgg ggc cgc ctc cac cat tgg ctg tac cgg ctc 538
 Ala Gly Pro Arg Thr Arg Gly Arg Leu His His Trp Leu Tyr Arg Leu 135
 125 130
 cag gag gcc cca aaa aag gag tcc cct ggc tgc ctc gag gcc tct gtc 586
 Gln Glu Ala Pro Lys Lys Glu Ser Pro Gly Cys Leu Glu Ala Ser Val 150
 140 145
 acc ttc aac ctc ttc cgc ctc ctc acg cga gac ctg aat tgt gtt gcc 634
 Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Asn Cys Val Ala 165
 155 160
 agt ggg gac ctg tgt gtc tga ccctcccacc agtcatgcaa cctgagattt 685
 Ser Gly Asp Leu Cys Val *
 170 175
 tatttataaaa ttagccactt gtcttaattt attgccaccc agtcgctat 734

<210> 18
 <211> 200
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> (1)...(25)

<400> 18
 Met Lys Leu Asp Met Thr Gly Asp Cys Thr Pro Val Leu Val Leu Met
 -25 -20 -15 -10
 Ala Ala Val Leu Thr Val Thr Gly Ala Val Pro Val Ala Arg Leu His
 -5 1 5
 Gly Ala Leu Pro Asp Ala Arg Gly Cys His Ile Ala Gln Phe Lys Ser
 10 15 20
 Leu Ser Pro Gln Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu
 25 30 35
 Glu Glu Ser Leu Leu Leu Lys Asp Cys Arg Cys His Ser Arg Leu Phe
 40 45 50 55
 Pro Arg Thr Trp Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Met
 60 65 70
 Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr
 75 80 85
 Ala Asp Thr Asp Pro Ala Leu Val Asp Val Leu Asp Gln Pro Leu His
 90 95 100
 Thr Leu His His Ile Leu Ser Gln Phe Arg Ala Cys Ile Gln Pro Gln
 105 110 115
 Pro Thr Ala Gly Pro Arg Thr Arg Gly Arg Leu His His Trp Leu Tyr
 120 125 130 135
 Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Pro Gly Cys Leu Glu Ala
 140 145 150
 Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Asn Cys
 155 160 165
 Val Ala Ser Gly Asp Leu Cys Val
 170 175

<210> 19

<211> 856
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> (98)...(154)

<221> mat_peptide
 <222> (155)...(700)

<221> CDS
 <222> (98)...(700)

<400> 19
 aattaccttt tcactttaca cacatcatct tggattgcc attttgctg gctaaaaagc 60
 agagccatgc cgctggggaa gcagttgcga tttagcc atg gct gca gct tgg acc 115
 Met Ala Ala Ala Trp Thr
 -15

gtg gtg ctg gtg act ttg gtg cta ggc ttg gcc gtg gca ggc cct gtc 163
 Val Val Leu Val Thr Leu Val Leu Gly Leu Ala Val Ala Gly Pro Val
 -10 -5 1

ccc act tcc aag ccc acc aca act ggg aag ggc tgc cac att ggc agg 211
 Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Cys His Ile Gly Arg
 5 10 15

ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag aag gcc agg 259
 Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg
 20 25 30 35

gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt tgc agc tct 307
 Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser
 40 45 50

cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag gtg agg gag 355
 Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu
 55 60 65

cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg aag gtc ctg 403
 Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu
 70 75 80

gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac cag ccc ctt 451
 Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu
 85 90 95

cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt atc cag cct 499
 His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro
 100 105 110 115

cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac cac tgg ctg 547
 Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu
 120 125 130

cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc tgc ctg gag 595
 His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu
 135 140 145

gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga gac ctc aaa 643
 Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys
 150 155 160

tat gtg gcc gat ggg aac ctg tgt ctg aga acg tca acc cac cct gag 691

Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser Thr His Pro Glu
 165 170 175

tcc acc tga caccacac cttatttatg cgctgagccc tactccttcc 740
 Ser Thr *
 180

ttaatttatt tcctctcacc ctttatttat gaagctgcag ccctgactga gacatagggc 800
 tgagtttatt gttttacttt tatacattat gcacaaataa acaacaagga attgga 856

<210> 20
 <211> 200
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> (1)...(19)

<400> 20
 Met Ala Ala Ala Trp Thr Val Val Leu Val Thr Leu Val Leu Gly Leu
 -15 -10 -5
 Ala Val Ala Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys
 1 5 10
 Gly Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala
 15 20 25
 Ser Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys
 30 35 40 45
 Asn Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg
 50 55 60
 Leu Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala
 65 70 75
 Leu Thr Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp
 80 85 90
 Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu
 95 100 105
 Gln Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly
 110 115 120 125
 Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu
 130 135 140
 Ser Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
 145 150 155
 Leu Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg
 160 165 170
 Thr Ser Thr His Pro Glu Ser Thr
 175 180

<210> 21
 <211> 734
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> (53)...(127)

<221> mat_peptide
 <222> (128)...(655)

<221> CDS
 <222> (53)...(655)

<400> 21
 tgggtgacag cctcagagt tttcttctgc tgacaaagac cagagatcag ga atg aaa 58

Met Lys
-25

cta gac atg acc ggg gac tgc atg cca gtg ctg gtg ctg atg gcc gca 106
 Leu Asp Met Thr Gly Asp Cys Met Pro Val Leu Val Leu Met Ala Ala
 -20 -15 -10

gtg ctg acc gtg act gga gca gtt cct gtc gcc agg ctc cgc ggg gct 154
 Val Leu Thr Val Thr Gly Ala Val Pro Val Ala Arg Leu Arg Gly Ala
 -5 1 5

ctc ccg gat gca agg ggc tgc cac ata gcc cag ttc aag tcc ctg tct 202
 Leu Pro Asp Ala Arg Gly Cys His Ile Ala Gln Phe Lys Ser Leu Ser
 10 15 20 25

cca cag gag ctg cag gcc ttt aag agg gcc aaa gat gcc tta gaa gag 250
 Pro Gln Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu
 30 35 40

tgc ctt ctg ctg aag gac tgc aag tgc cgc tcc cgc ctc ttc ccc agg 298
 Ser Leu Leu Leu Lys Asp Cys Lys Cys Arg Ser Arg Leu Phe Pro Arg
 45 50 55

acc tgg gac ctg agg cag ctg cag gtg agg gag cgc ccc gtg gct ttg 346
 Thr Trp Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Val Ala Leu
 60 65 70

gag gct gag ctg gcc ctg acg ctg aag gtt ctg gag gcc acc gct gac 394
 Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr Ala Asp
 75 80 85

act gac cca gcc ctg ggg gat gtc ttg gac cag ccc ctt cac acc ctg 442
 Thr Asp Pro Ala Leu Gly Asp Val Leu Asp Gln Pro Leu His Thr Leu
 90 95 100 105

cac cat atc ctc tcc cag ctc cgg gcc tgt atc cag cct cag ccc acg 490
 His His Ile Leu Ser Gln Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr
 110 115 120

gca ggg ccc agg acc cgg ggc cgc ctc cac cat tgg ctg cac cgg ctc 538
 Ala Gly Pro Arg Thr Arg Gly Arg Leu His His Trp Leu His Arg Leu
 125 130 135

cag gag gcc cca aaa aag gag tcc cct ggc tgc ctc gag gcc tct gtc 586
 Gln Glu Ala Pro Lys Lys Glu Ser Pro Gly Cys Leu Glu Ala Ser Val
 140 145 150

acc ttc aac ctc ttc cgc ctc ctc acg cga gac ctg aat tgt gtt gcc 634
 Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Asn Cys Val Ala
 155 160 165

agc ggg gac ctg tgt gtc tga cccttcgcc agtcatgcaa cctgagattt 685
 Ser Gly Asp Leu Cys Val *

tatttataaaa ttagccactt ggcttaattt attgccaccc agtcgctat 734

<210> 22
 <211> 200
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> (1)...(25)

<400> 22
 Met Lys Leu Asp Met Thr Gly Asp Cys Met Pro Val Leu Val Leu Met
 -25 -20 -15 -10
 Ala Ala Val Leu Thr Val Thr Gly Ala Val Pro Val Ala Arg Leu Arg
 -5 1 5
 Gly Ala Leu Pro Asp Ala Arg Gly Cys His Ile Ala Gln Phe Lys Ser
 10 15 20
 Leu Ser Pro Gln Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu
 25 30 35
 Glu Glu Ser Leu Leu Lys Asp Cys Lys Cys Arg Ser Arg Leu Phe
 40 45 50 55
 Pro Arg Thr Trp Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Val
 60 65 70
 Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr
 75 80 85
 Ala Asp Thr Asp Pro Ala Leu Gly Asp Val Leu Asp Gln Pro Leu His
 90 95 100
 Thr Leu His His Ile Leu Ser Gln Leu Arg Ala Cys Ile Gln Pro Gln
 105 110 115
 Pro Thr Ala Gly Pro Arg Thr Arg Gly Arg Leu His His Trp Leu His
 120 125 130 135
 Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Pro Gly Cys Leu Glu Ala
 140 145 150
 Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Asn Cys
 155 160 165
 Val Ala Ser Gly Asp Leu Cys Val
 170 175

<210> 23
 <211> 528
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IL-28A mutant C48S

<221> CDS
 <222> (1)...(528)

<400> 23
 gtt cct gtc gcc agg ctc cac ggg gct ctc ccg gat gca agg ggc tgc 48
 Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly Cys
 1 5 10 15
 cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc ttt 96
 His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe
 20 25 30
 aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac tcc 144
 Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp Ser
 35 40 45
 agg tgc cac tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag ctg 192
 Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu
 50 55 60
 cag gtg agg gag cgc ccc atg gct ttg gag gct gag ctg gcc ctg acg 240
 Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg gtg gac 288
 Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val Asp
 85 90 95

gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag ttc 336
 Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Phe
 100 105 110

cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg ggc 384
 Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly
 115 120 125

cgc ctc cac cat tgg ctg tac cgg ctc cag gag gcc cca aaa aag gag 432
 Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu
 130 135 140

tcc cct gcc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc ctc 480
 Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
 145 150 155 160

ctc acg cga gac ctg aat tgt gtt gcc agt ggg gac ctg tgt gtc tga 528
 Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val *
 165 170 175

<210> 24
 <211> 175
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IL-28A mutant C48S

<400> 24
 Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly Cys
 1 5 10 15
 His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe
 20 25 30
 Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp Ser
 35 40 45
 Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu
 50 55 60
 Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val Asp
 85 90 95
 Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Phe
 100 105 110
 Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly
 115 120 125
 Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu
 130 135 140
 Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
 145 150 155 160
 Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175

<210> 25
 <211> 531
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> met IL-28A mutant C49S

<221> CDS

<222> (1)...(531)

<400> 25

atg gtt cct gtc gcc agg ctc cac ggg gct ctc ccg gat gca agg ggc	48
Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly	
1 5 10 15	
tgc cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc	96
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala	
20 25 30	
ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac	144
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp	
35 40 45	
tcc agg tgc cac tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag	192
Ser Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln	
50 55 60	
ctg cag gtg agg gag cgc ccc atg gct ttg gag gct gag ctg gcc ctg	240
Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu	
65 70 75 80	
acg ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg gtg	288
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val	
85 90 95	
gac gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag	336
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln	
100 105 110	
ttc cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg	384
Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg	
115 120 125	
ggc cgc ctc cac cat tgg ctg tac cgg ctc cag gag gcc cca aaa aag	432
Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys	
130 135 140	
gag tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc	480
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg	
145 150 155 160	
ctc ctc acg cga gac ctg aat tgt gtt gcc agt ggg gac ctg tgt gtc	528
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val	
165 170 175	
tga	531
*	

<210> 26

<211> 176

<212> PRT

<213> Artificial Sequence

<220>

<223> met IL-28A mutant C49S

<400> 26

Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly	
1 5 10 15	
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala	
20 25 30	

Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
 35 40 45
 Ser Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
 50 55 60
 Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu
 65 70 75 80
 Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val
 85 90 95
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
 100 105 110
 Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
 115 120 125
 Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
 130 135 140
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
 145 150 155 160
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175

<210> 27
 <211> 528
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IL-28A mutant C50S

<221> CDS
 <222> (1)...(528)

<400> 27
 gtt cct gtc gcc agg ctc cac ggg gct ctc ccg gat gca agg ggc tgc 48
 Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly Cys
 1 5 10 15
 cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc ttt 96
 His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe
 20 25 30
 aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac tgc 144
 Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp Cys
 35 40 45
 agg tcc cac tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag ctg 192
 Arg Ser His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu
 50 55 60
 cag gtg agg gag cgc ccc atg gct ttg gag gct gag ctg gcc ctg acg 240
 Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg gtg gac 288
 Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val Asp
 85 90 95
 gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag ttc 336
 Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Phe
 100 105 110
 cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg ggc 384
 Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly
 115 120 125
 cgc ctc cac cat tgg ctg tac cgg ctc cag gag gcc cca aaa aag gag 432

Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu
 130 135 140

tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc ctc 480
 Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
 145 150 155 160

ctc acg cga gac ctg aat tgt gtt gcc agt ggg gac ctg tgt gtc tga 528
 Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val *
 165 170 175

<210> 28

<211> 175

<212> PRT

<213> Artificial Sequence

<220>

<223> IL-28A mutant C50S

<400> 28

Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly Cys
 1 5 10 15
 His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe
 20 25 30
 Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp Cys
 35 40 45
 Arg Ser His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu
 50 55 60
 Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val Asp
 85 90 95
 Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Phe
 100 105 110
 Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly
 115 120 125
 Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu
 130 135 140
 Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
 145 150 155 160
 Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175

<210> 29

<211> 531

<212> DNA

<213> Artificial Sequence

<220>

<223> met IL-28A mutant C51S

<221> CDS

<222> (1)...(531)

<400> 29

atg gtt cct gtc gcc agg ctc cac ggg gct ctc ccg gat gca agg ggc 48
 Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly
 1 5 10 15
 tgc cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc 96
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
 20 25 30

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ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac 144
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
      35              40              45

tgc agg tcc cac tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag 192
Cys Arg Ser His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
      50              55              60

ctg cag gtg agg gag cgc ccc atg gct ttg gag gct gag ctg gcc ctg 240
Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu
      65              70              75              80

acg ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg gtg 288
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val
      85              90              95

gac gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag 336
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
      100              105              110

ttc cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg 384
Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
      115              120              125

ggc cgc ctc cac cat tgg ctg tac cgg ctc cag gag gcc cca aaa aag 432
Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
      130              135              140

gag tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc 480
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
      145              150              155              160

ctc ctc acg cga gac ctg aat tgt gtt gcc agt ggg gac ctg tgt gtc 528
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
      165              170              175

tga 531
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<210> 30
 <211> 176
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> met IL-28A mutant C51S

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<400> 30
Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly
1      5      10      15
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
20     25     30
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp
35     40     45
Cys Arg Ser His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
50     55     60
Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu
65     70     75     80
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val
85     90     95
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
100    105    110
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Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
 115 120 125
 Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
 130 135 140
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
 145 150 155 160
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175

<210> 31

<211> 546

<212> DNA

<213> Artificial Sequence

<220>

<223> IL-29 mutant C171S

<221> CDS

<222> (1).....(546)

<400> 31

ggt ccg gtt ccg acc tct aaa cca acc acc act ggt aaa ggt tgc cac 48
 Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His
 1 5 10 15
 atc ggt cgt ttc aaa tct ctg tct ccg cag gaa ctg gct tct ttc aaa 96
 Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
 20 25 30
 aaa gct cgt gac gct ctg gaa gaa tct ctg aaa ctg aaa aac tgg tct 144
 Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
 35 40 45
 tgc tct tct ccg gtt ttc ccg ggt aac tgg gat ctg cgt ctg ctg cag 192
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
 50 55 60
 gtt cgt gaa cgt ccg gtt gct ctg gaa gct gaa ctg gct ctg acc ctg 240
 Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
 65 70 75 80
 aaa gtt ctg gaa gct gct gca ggt cct gct ctg gaa gat gtt ctg gat 288
 Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
 85 90 95
 cag ccg ctg cac act ctg cac cac atc ctg tct cag ctg cag gct tgc 336
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
 100 105 110
 att caa ccg caa ccg acc gct ggt ccg cgt ccg cgt ggt cgt ctg cac 384
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
 115 120 125
 cac tgg ctg cat cgt ctg cag gaa gct ccg aaa aaa gaa tct gct ggt 432
 His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
 130 135 140
 tgc ctg gaa gct tct gtt acc ttc aac ctg ttc cgt ctg ctg acc cgt 480
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
 145 150 155 160
 gat ctg aaa tac gtt gct gat ggt aac ctg tct ctg cgt acc tct acc 528
 Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Ser Leu Arg Thr Ser Thr
 165 170 175

cat ccg gaa tct acc taa
His Pro Glu Ser Thr *
180

<210> 32
<211> 181
<212> PRT
<213> Artificial Sequence

<220>
<223> IL-29 mutant C171S

<400> 32
Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His
1 5 10 15
Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
20 25 30
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
35 40 45
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
50 55 60
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
65 70 75 80
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
85 90 95
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
100 105 110
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
115 120 125
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
130 135 140
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
145 150 155 160
Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Ser Leu Arg Thr Ser Thr
165 170 175
His Pro Glu Ser Thr
180

<210> 33
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> met IL-29 mutant C172S

<221> CDS
<222> (1)...(549)

<400> 33
atg ggt ccg gtt ccg acc tct aaa cca acc acc act ggt aaa ggt tgc 48
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys
1 5 10 15
cac atc ggt cgt ttc aaa tct ctg tct ccg cag gaa ctg gct tct ttc 96
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
20 25 30
aaa aaa gct cgt gac gct ctg gaa gaa tct ctg aaa ctg aaa aac tgg 144
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
35 40 45

tct tgc tct tct ccg gtt ttc ccg ggt aac tgg gat ctg cgt ctg ctg 192
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
 50 55 60
 cag gtt cgt gaa cgt ccg gtt gct ctg gaa gct gaa ctg gct ctg acc 240
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 ctg aaa gtt ctg gaa gct gct gca ggt cct gct ctg gaa gat gtt ctg 288
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95
 gat cag ccg ctg cac act ctg cac cac atc ctg tct cag ctg cag gct 336
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
 100 105 110
 tgc att caa ccg caa ccg acc gct ggt ccg cgt ccg cgt ggt cgt ctg 384
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125
 cac cac tgg ctg cat cgt ctg cag gaa gct ccg aaa aaa gaa tct gct 432
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140
 ggt tgc ctg gaa gct tct gtt acc ttc aac ctg ttc cgt ctg ctg acc 480
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160
 cgt gat ctg aaa tac gtt gct gat ggt aac ctg tct ctg cgt acc tct 528
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Ser Leu Arg Thr Ser
 165 170 175
 acc cat ccg gaa tct acc taa 549
 Thr His Pro Glu Ser Thr *
 180

<210> 34
 <211> 182
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> met IL-29 mutant C172S

<400> 34
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys
 1 5 10 15
 His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
 20 25 30
 Lys Lys Ala Arg Asp Ala Leu Glu Ser Leu Lys Leu Lys Asn Trp
 35 40 45
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
 50 55 60
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
 100 105 110
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr

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<221> CDS
<222> (1)...(531)
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[illegible]

<210> 36
 <211> 176
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> met IL-28A

<400> 36
 Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly
 1 5 10 15
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
 20 25 30
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
 35 40 45
 Cys Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
 50 55 60
 Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu
 65 70 75 80
 Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val
 85 90 95
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
 100 105 110
 Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
 115 120 125
 Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
 130 135 140
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
 145 150 155 160
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175

<210> 37
 <211> 621
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> met IL-29
 <221> CDS
 <222> (1)...(549)

<400> 37
 atg ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc tgc 48
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys
 1 5 10 15
 cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc 96
 His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
 20 25 30
 aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg 144
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
 35 40 45
 agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc 192
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
 50 55 60
 cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg 240

Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80

ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta 288
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95

gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc 336
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
 100 105 110

tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc 384
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125

cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct 432
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140

ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg 480
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160

cga gac ctc aaa tat gtg gcc gat ggg aac ctg tgt ctg aga acg tca 528
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser
 165 170 175

acc cac cct gag tcc acc tga caccacac cttatttatg cgctgagccc 579
 Thr His Pro Glu Ser Thr *
 180

tactccttcc-ttaatttatt tcctctcacc-ctttatttat ga 621

<210> 38

<211> 182

<212> PRT

<213> Artificial Sequence

<220>

<223> met IL-29

<400> 38

Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys
 1 5 10 15
 His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
 20 25 30
 Lys Lys Ala Arg Asp Ala Leu Glu Ser Leu Lys Leu Lys Asn Trp
 35 40 45
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
 50 55 60
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
 100 105 110
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser
 165 170 175
 Thr His Pro Glu Ser Thr

180

<210> 39
 <211> 531
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> met IL-28B

<221> CDS
 <222> (1)...(531)

<400> 39
 atg gtt cct gtc gcc agg ctc cgc ggg gct ctc ccg gat gca agg ggc 48
 Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
 1 5 10 15

tgc cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc 96
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
 20 25 30

ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac 144
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
 35 40 45

tgc aag tgc cgc tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag 192
 Cys Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
 50 55 60

ctg cag gtg agg gag cgc ccc gtg gct ttg gag gct gag ctg gcc ctg 240
 Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
 65 70 75 80

acg ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg ggg 288
 Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Gly
 85 90 95

gat gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag 336
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
 100 105 110

ctc cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg 384
 Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
 115 120 125

ggc cgc ctc cac cat tgg ctg cac cgg ctc cag gag gcc cca aaa aag 432
 Gly Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys
 130 135 140

gag tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc 480
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
 145 150 155 160

ctc ctc acg cga gac ctg aat tgt gtt gcc agc ggg gac ctg tgt gtc 528
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175

tga 531
 *

<210> 40

<211> 176
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> met IL-28B

<400> 40
 Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
 1 5 10 15
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
 20 25 30
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp
 35 40 45
 Cys Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
 50 55 60
 Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
 65 70 75 80
 Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Gly
 85 90 95
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
 100 105 110
 Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
 115 120 125
 Gly Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys
 130 135 140
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
 145 150 155 160
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175

<210> 41
 <211> 546
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IL-29 Cys15 mutant, Asn169

<221> CDS
 <222> (1)...(546)

<221> variation
 <222> (44)...(45)
 <223> n = A, T, G, or C

<400> 41
 ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc dnn cac 48
 Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa His
 1 5 10 15
 att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag 96
 Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
 20 25 30
 aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt 144
 Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
 35 40 45
 tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag 192
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
 50 55 60
 gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg 240

Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
 65 70 75 80

aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac 288
 Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
 85 90 95

cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt 336
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
 100 105 110

atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac 384
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
 115 120 125

cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc 432
 His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
 130 135 140

tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga 480
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
 145 150 155 160

gac ctc aaa tat gtg gcc gat ggg aay ctg tgt ctg aga acg tca acc 528
 Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser Thr
 165 170 175

cac cct gag tcc acc tga 546
 His Pro Glu Ser Thr *

<210> 42

<211> 181

<212> PRT

<213> Artificial Sequence

<220>

<223> IL-29 Cys15 mutant, Asn169

<221> VARIANT

<222> (15)...(15)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 42

Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa His
 1 5 10 15

Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
 20 25 30

Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
 35 40 45

Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
 50 55 60

Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
 65 70 75 80

Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
 85 90 95

Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
 100 105 110

Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
 115 120 125

His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
 130 135 140

Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
 145 150 155 160

Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser Thr
 165 170 175
 His Pro Glu Ser Thr
 180

<210> 43
 <211> 549
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Met IL-29 Cys16 mutant, Asn170

<221> CDS
 <222> (1)...(549)

<221> variation
 <222> (47)...(48)
 <223> n = A, T, G, or C

<400> 43
 atg ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc dnn 48
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa
 1 5 10 15
 cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc 96
 His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
 20 25 30
 aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg 144
 Lys Lys Ala Arg Asp Ala Leu Glu Ser Leu Lys Leu Lys Asn Trp
 35 40 45
 agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc 192
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
 50 55 60
 cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg 240
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta 288
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95
 gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc 336
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
 100 105 110
 tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc 384
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125
 cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct 432
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140
 ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg 480
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160
 cga gac ctc aaa tat gtg gcc gat ggg aay ctg tgt ctg aga acg tca 528
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser
 165 170 175

acc cac cct gag tcc acc tga
 Thr His Pro Glu Ser Thr *
 180

<210> 44
 <211> 182
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Met IL-29 Cys16 mutant, Asn170

<221> VARIANT
 <222> (16)...(16)
 <223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 44
 Met Gly-Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa
 1 5 10 15
 His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
 20 25 30
 Lys Lys Ala Arg Asp Ala Leu Glu Ser Leu Lys Leu Lys Asn Trp
 35 40 45
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
 50 55 60
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
 100 105 110
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser
 165 170 175
 Thr His Pro Glu Ser Thr
 180

<210> 45
 <211> 546
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IL-29 Cys15 mutant, Asp169

<221> CDS
 <222> (1)...(546)

<221> variation
 <222> (44)...(45)
 <223> n = A, T, G, or C

<400> 45
 ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc dnn cac 48
 Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa His
 1 5 10 15

att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag 96
 Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
 20 25 30

aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt 144
 Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
 35 40 45

tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag 192
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
 50 55 60

gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg 240
 Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
 65 70 75 80

aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac 288
 Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
 85 90 95

cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt 336
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
 100 105 110

atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac 384
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
 115 120 125

cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc 432
 His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
 130 135 140

tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga 480
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
 145 150 155 160

gac ctc aaa tat gtg gcc gat ggg gay ctg tgt ctg aga acg tca acc 528
 Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser Thr
 165 170 175

cac cct gag tcc acc tga 546
 His Pro Glu Ser Thr *
 180

<210> 46

<211> 181

<212> PRT

<213> Artificial Sequence

<220>

<223> IL-29 Cys15 mutant, Asp169

<221> VARIANT

<222> (15)...(15)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 46

Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa His
 1 5 10 15
 Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
 20 25 30
 Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
 35 40 45
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln

50	55	60
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu		
65	70	75
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp		80
	85	90
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys		95
	100	105
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His		110
	115	120
His Trp Leu His His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly		125
	130	135
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg		140
145	150	155
Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser Thr		160
	165	170
His Pro Glu Ser Thr		175
	180	

<210> 47

<211> 549

<212> DNA

<213> Artificial Sequence

<220>

<223> Met IL-29 Cys16 mutant, Asp170

<221> CDS

<222> (1)...(549)

<221> variation

<222> (47)...(48)

<223> n = A, T, G, or C

<400> 47

atg ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc dnn	48
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa	
1 5 10 15	

cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc	96
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe	
20 25 30	

aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg	144
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp	
35 40 45	

agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc	192
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu	
50 55 60	

cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg	240
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr	
65 70 75 80	

ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta	288
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu	
85 90 95	

gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc	336
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala	
100 105 110	

tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc	384
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu	

115	120	125	
cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct			432
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala			
130	135	140	
ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg			480
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr			
145	150	155	160
cga gac ctc aaa tat gtg gcc gat ggg gay ctg tgt ctg aga acg tca			528
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser			
165	170	175	
acc cac cct gag tcc acc tga			549
Thr His Pro Glu Ser Thr *			
180			

<210> 48
 <211> 182
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Met IL-29 Cys16 mutant., Asp170

 <221> VARIANT
 <222> (16)...(16)
 <223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 48	
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa	
1	15
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe	
20	30
Lys Lys Ala Arg Asp Ala Leu Glu Ser Leu Lys Leu Lys Asn Trp	
35	45
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu	
50	60
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr	
65	80
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu	
85	95
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala	
100	110
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu	
115	125
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala	
130	140
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr	
145	160
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser	
165	175
Thr His Pro Glu Ser Thr	
180	

<210> 49
 <211> 546
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> IL-29 Asp169 Cys171 mutant

<221> CDS

<222> (1)...(546)

<221> variation

<222> (512)...(513)

<223> n = A, T, G, or C

<400> 49

```

ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc tgc cac 48
Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His
1           5           10           15

```

```

att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag 96
Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
           20           25           30

```

```

aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt 144
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
           35           40           45

```

```

tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag 192
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
           50           55           60

```

```

gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg 240
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
           65           70           75           80

```

```

aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac 288
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
           85           90           95

```

```

cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt 336
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
           100           105           110

```

```

atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac 384
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
           115           120           125

```

```

cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc 432
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
           130           135           140

```

```

tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga 480
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
           145           150           155           160

```

```

gac ctc aaa tat gtg gcc gat ggg gay ctg dnn ctg aga acg tca acc 528
Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Xaa Leu Arg Thr Ser Thr
           165           170           175

```

```

cac cct gag tcc acc tga 546
His Pro Glu Ser Thr *
           180

```

<210> 50

<211> 181

<212> PRT

<213> Artificial Sequence

<220>

<223> IL-29 Asp169 Cys171 mutant

<221> VARIANT

<222> (171)...(171)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 50

Gly	Pro	Val	Pro	Thr	Ser	Lys	Pro	Thr	Thr	Thr	Gly	Lys	Gly	Cys	His
1				5				10						15	
Ile	Gly	Arg	Phe	Lys	Ser	Leu	Ser	Pro	Gln	Glu	Leu	Ala	Ser	Phe	Lys
			20					25					30		
Lys	Ala	Arg	Asp	Ala	Leu	Glu	Glu	Ser	Leu	Lys	Leu	Lys	Asn	Trp	Ser
		35					40					45			
Cys	Ser	Ser	Pro	Val	Phe	Pro	Gly	Asn	Trp	Asp	Leu	Arg	Leu	Leu	Gln
	50				55					60					
Val	Arg	Glu	Arg	Pro	Val	Ala	Leu	Glu	Ala	Glu	Leu	Ala	Leu	Thr	Leu
65					70				75					80	
Lys	Val	Leu	Glu	Ala	Ala	Ala	Gly	Pro	Ala	Leu	Glu	Asp	Val	Leu	Asp
			85					90						95	
Gln	Pro	Leu	His	Thr	Leu	His	His	Ile	Leu	Ser	Gln	Leu	Gln	Ala	Cys
		100						105					110		
Ile	Gln	Pro	Gln	Pro	Thr	Ala	Gly	Pro	Arg	Pro	Arg	Gly	Arg	Leu	His
		115					120					125			
His	Trp	Leu	His	Arg	Leu	Gln	Glu	Ala	Pro	Lys	Lys	Glu	Ser	Ala	Gly
	130					135					140				
Cys	Leu	Glu	Ala	Ser	Val	Thr	Phe	Asn	Leu	Phe	Arg	Leu	Leu	Thr	Arg
145					150					155					160
Asp	Leu	Lys	Tyr	Val	Ala	Asp	Gly	Asp	Leu	Xaa	Leu	Arg	Thr	Ser	Thr
			165					170						175	
His	Pro	Glu	Ser	Thr											
			180												

<210> 51

<211> 549

<212> DNA

<213> Artificial Sequence

<220>

<223> Met IL-29 Asp170 Cys172 mutant

<221> CDS

<222> (1)...(549)

<221> variation

<222> (515)...(516)

<223> n = A, T, G, or C

<400> 51

atg	ggc	cct	gtc	ccc	act	tcc	aag	ccc	acc	aca	act	ggg	aag	ggc	tgc	48
Met	Gly	Pro	Val	Pro	Thr	Ser	Lys	Pro	Thr	Thr	Thr	Gly	Lys	Gly	Cys	
1				5				10						15		
cac	att	ggc	agg	ttc	aaa	tct	ctg	tca	cca	cag	gag	cta	gcg	agc	ttc	96
His	Ile	Gly	Arg	Phe	Lys	Ser	Leu	Ser	Pro	Gln	Glu	Leu	Ala	Ser	Phe	
			20					25					30			
aag	aag	gcc	agg	gac	gcc	ttg	gaa	gag	tca	ctc	aag	ctg	aaa	aac	tgg	144
Lys	Lys	Ala	Arg	Asp	Ala	Leu	Glu	Glu	Ser	Leu	Lys	Leu	Lys	Asn	Trp	
		35				40					45					
agt	tgc	agc	tct	cct	gtc	ttc	ccc	ggg	aat	tgg	gac	ctg	agg	ctt	ctc	192
Ser	Cys	Ser	Ser	Pro	Val	Phe	Pro	Gly	Asn	Trp	Asp	Leu	Arg	Leu	Leu	
	50					55				60						
cag	gtg	agg	gag	cgc	cct	gtg	gcc	ttg	gag	gct	gag	ctg	gcc	ctg	acg	240

Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
65 70 75 80

ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta 288
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu 95

gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc 336
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala 110
100 105

tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc 384
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu 125
115 120

cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct 432
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala 140
130 135

ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg 480
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr 160
145 150 155

cga gac ctc aaa tat gtg gcc gat ggg gag ctg dnn ctg aga acg tca 528
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Xaa Leu Arg Thr Ser 175
165 170

acc cac cct gag tcc acc tga 549
Thr His Pro Glu Ser Thr *
180

<210> 52

<211> 182

<212> PRT

<213> Artificial Sequence

<220>

<223> Met IL-29 Asp170 Cys172 mutant

<221> VARIANT

<222> (172)...(172)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 52

Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys
1 5 10 15
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
20 25 30
Lys Lys Ala Arg Asp Ala Leu Glu Ser Leu Lys Leu Lys Asn Trp
35 40 45
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
50 55 60
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
65 70 75 80
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
85 90 95
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
100 105 110
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
115 120 125
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
130 135 140
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145 150 155 160

Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Xaa Leu Arg Thr Ser
 165 170 175
 Thr His Pro Glu Ser Thr
 180

<210> 53
 <211> 546
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IL-29 Pro10 Asn169 Cys171 mutant

<221> CDS
 <222> (1)...(546)

<221> variation
 <222> (30)...(30)
 <223> n = A, T, G, or C

<221> variation
 <222> (512)...(513)
 <223> n = A, T, G, or C

<400> 53
 ggc cct gtc ccc act tcc aag ccc acc ccn act ggg aag ggc tgc cac 48
 Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Cys His
 1 5 10 15
 att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag 96
 Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
 20 25 30
 aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt 144
 Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
 35 40 45
 tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag 192
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
 50 55 60
 gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg 240
 Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
 65 70 75 80
 aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac 288
 Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
 85 90 95
 cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt 336
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
 100 105 110
 atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac 384
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
 115 120 125
 cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc 432
 His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
 130 135 140
 tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga 480
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
 145 150 155 160

gac ctc aaa tat gtg gcc gat ggg aac ctg dnn ctg aga acg tca acc 528
 Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr
 165 170 175

cac cct gag tcc acc tga 546
 His Pro Glu Ser Thr *
 180

<210> 54
 <211> 181
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IL-29 Pro10 Asn169 Cys171 mutant

<221> VARIANT
 <222> (171)... (171)
 <223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 54
 Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Cys His
 1 5 10 15
 Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
 20 25 30
 Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
 35 40 45
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
 50 55 60
 Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
 65 70 75 80
 Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
 85 90 95
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
 100 105 110
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
 115 120 125
 His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
 130 135 140
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
 145 150 155 160
 Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr
 165 170 175
 His Pro Glu Ser Thr
 180

<210> 55
 <211> 549
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Met IL-29 Pro11 Asn170 Cys172 mutant

<221> CDS
 <222> (1)... (549)

<221> variation
 <222> 33, 515, 516
 <223> n = A, T, G, or C

<400> 55

atg ggc cct gtc ccc act tcc aag ccc acc ccn act ggg aag ggc tgc 48
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Cys
 1 5 10 15
 cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc 96
 His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
 20 25 30
 aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg 144
 Lys Lys Ala Arg Asp Ala Leu Glu Ser Leu Lys Leu Lys Asn Trp
 35 40 45
 agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc 192
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
 50 55 60
 cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg 240
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta 288
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95
 gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc 336
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
 100 105 110
 tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc 384
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125
 cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct 432
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140
 ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg 480
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160
 cga gac ctc aaa tat gtg gcc gat ggg aac ctg dnn ctg aga acg tca 528
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser
 165 170 175
 acc cac cct gag tcc acc tga 549
 Thr His Pro Glu Ser Thr *
 180

<210> 56

<211> 182

<212> PRT

<213> Artificial Sequence

<220>

<223> Met .IL-29 Pro11 Asn170 Cys172 mutant

<221> VARIANT

<222> (172)...(172)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 56

Met Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Cys
 1 5 10 15
 His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe

20 25 30
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
 35 40 45
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
 50 55 60
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
 100 105 110
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser
 165 170 175
 Thr His Pro Glu Ser Thr
 180

<210> 57
 <211> 546
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IL-29 Pro10 Cys15 mutant Asn169

<221> CDS
 <222> (1)...(546)

<221> variation
 <222> (30)...(30)
 <223> n = A, T, G, or C

<221> variation
 <222> (44)...(45)
 <223> n = A, T, G, or C

<400> 57
 ggc cct gtc ccc act tcc aag ccc acc ccn act ggg aag ggc dnn cac 48
 Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Xaa His
 1 5 10 15

att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag 96
 Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
 20 25 30

aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt 144
 Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
 35 40 45

tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag 192
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
 50 55 60

gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg 240
 Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
 65 70 75 80

aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac 288
 Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp

85

90

95

cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt 336
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
 100 105 110

atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac 384
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
 115 120 125

cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc 432
 His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
 130 135 140

tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga 480
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
 145 150 155 160

gac ctc aaa tat gtg gcc gat ggg aay ctg tgt ctg aga acg tca acc 528
 Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser Thr
 165 170 175

cac cct gag tcc acc tga 546
 His Pro Glu Ser Thr *

<210> 58

<211> 181

<212> PRT

<213> Artificial Sequence

<220>

<223> IL-29 Pro10 Cys15 mutant Asn169

<221> VARIANT

<222> (15)...(15)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 58

Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Xaa His
 1 5 10 15
 Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
 20 25 30
 Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
 35 40 45
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
 50 55 60
 Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
 65 70 75 80
 Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
 85 90 95
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
 100 105 110
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
 115 120 125
 His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
 130 135 140
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
 145 150 155 160
 Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser Thr
 165 170 175
 His Pro Glu Ser Thr
 180

<210> 59
 <211> 549
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Met IL-29 Pro11 Cys16 mutant Asn170

<221> CDS
 <222> (1)...(549)

<221> variation
 <222> (33)...(33)
 <223> n = A, T, G, or C

<221> variation
 <222> (47)...(48)
 <223> n = A, T, G, or C

<400> 59
 atg ggc cct gtc ccc act tcc aag ccc acc ccn act ggg aag ggc dnn 48
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Xaa
 1 5 10 15
 cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc 96
 His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
 20 25 30
 aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg 144
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
 35 40 45
 agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc 192
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
 50 55 60
 cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg 240
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta 288
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95
 gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc 336
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
 100 105 110
 tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc 384
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125
 cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct 432
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140
 ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg 480
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160
 cga gac ctc aaa tat gtg gcc gat ggg aay ctg tgt ctg aga acg tca 528
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser
 165 170 175

acc cac cct gag tcc acc tga
 Thr His Pro Glu Ser Thr *
 180

549

<210> 60
 <211> 182
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Met_IL-29_Pro11 Cys16 mutant Asn170

<221> VARIANT
 <222> (16)...(16)
 <223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 60
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Xaa
 1 5 10 15
 His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
 20 25 30
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
 35 40 45
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
 50 55 60
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
 100 105 110
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser
 165 170 175
 Thr His Pro Glu Ser Thr
 180

<210> 61
 <211> 546
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IL-29 Pro10 Asp169 Cys171 mutant

<221> CDS
 <222> (1)...(546)

<221> variation
 <222> (30)...(30)
 <223> n = A, T, G, or C

<221> variation
 <222> (512)...(513)
 <223> n = A, T, G, or C

<400> 61
 ggc cct gtc ccc act tcc aag ccc acc ccn act ggg aag ggc tgc cac 48

Gly	Pro	Val	Pro	Thr	Ser	Lys	Pro	Thr	Pro	Thr	Gly	Lys	Gly	Cys	His	
1				5					10					15		
att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag																96
Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys																
		20					25					30				
aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt																144
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser																
		35				40						45				
tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag																192
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln																
		50				55				60						
gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg																240
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu																
		65			70				75					80		
aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac																288
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp																
				85			90						95			
cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt																336
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys																
			100				105						110			
atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac																384
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His																
			115				120					125				
cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc																432
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly																
		130				135				140						
tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga																480
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg																
		145			150				155					160		
gac ctc aaa tat gtg gcc gat ggg gay ctg dnn ctg aga acg tca acc																528
Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Xaa Leu Arg Thr Ser Thr																
			165				170						175			
cac cct gag tcc acc tga																546
His Pro Glu Ser Thr *																
			180													

<210> 62

<211> 181

<212> PRT

<213> Artificial Sequence

<220>

<223> IL-29 Pro10 Asp169 Cys171 mutant

<221> VARIANT

<222> (171)...(171)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 62

Gly	Pro	Val	Pro	Thr	Ser	Lys	Pro	Thr	Pro	Thr	Gly	Lys	Gly	Cys	His	
1				5					10					15		
Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys																
		20					25						30			

Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
 35 40 45
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
 50 55 60
 Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
 65 70 75 80
 Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
 85 90 95
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
 100 105 110
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
 115 120 125
 His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
 130 135 140
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
 145 150 155 160
 Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Xaa Leu Arg Thr Ser Thr
 165 170 175
 His Pro Glu Ser Thr
 180

<210> 63
 <211> 549
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Met IL-29 Pro11 Asp170 Cys172 mutant

<221> CDS
 <222> (1)...(549)

<221> variation
 <222> (33)...(33)
 <223> n = A, T, G, or C

<221> variation
 <222> (515)...(516)
 <223> n = A, T, G, or C

<400> 63
 atg ggc cct gtc ccc act tcc aag ccc acc ccn act ggg aag ggc tgc 48
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Cys
 1 5 10 15

cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc 96
 His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
 20 25 30

aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg 144
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
 35 40 45

agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc 192
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
 50 55 60

cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg 240
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80

ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta 288
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95

gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc 336
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
 100 105 110

tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc 384
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125

cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct 432
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140

ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg 480
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160

cga gac ctc aaa tat gtg gcc gat ggg gay ctg dnn ctg aga acg tca 528
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Xaa Leu Arg Thr Ser
 165 170 175

acc cac cct gag tcc acc tga 549
 Thr His Pro Glu Ser Thr *

<210> 64

<211> 182

<212> PRT

<213> Artificial Sequence

<220>

<223> Met IL-29 Pro11 Asp170 Cys172 mutant

<221> VARIANT

<222> (172) ... (172)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 64

Met Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Cys
 1 5 10 15
 His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
 20 25 30
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
 35 40 45
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
 50 55 60
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
 100 105 110
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Xaa Leu Arg Thr Ser
 165 170 175
 Thr His Pro Glu Ser Thr
 180

<210> 65
 <211> 546
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IL-29 Pro10 Cys15 mutant Asp169

<221> CDS
 <222> (1)...(546)

<221> variation
 <222> 30, 44, 45
 <223> n = A, T, G, or C

<400> 65

ggc cct gtc ccc act tcc aag ccc acc ccn act ggg aag ggc dnn cac	48
Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Xaa His	
1 5 10 15	
att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag	96
Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys	
20 25 30	
aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt	144
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser	
35 40 45	
tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag	192
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln	
50 55 60	
gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg	240
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu	
65 70 75 80	
aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac	288
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp	
85 90 95	
cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt	336
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys	
100 105 110	
atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac	384
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His	
115 120 125	
cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc	432
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly	
130 135 140	
tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga	480
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg	
145 150 155 160	
gac ctc aaa tat gtg gcc gat ggg gay ctg tgt ctg aga acg tca acc	528
Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser Thr	
165 170 175	
cac cct gag tcc acc tga	546
His Pro Glu Ser Thr *	
180	

<210> 66
 <211> 181
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IL-29 Pro10 Cys15 mutant Asp169

<221> VARIANT
 <222> (15)...(15)
 <223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 66
 Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Xaa His
 1 5 10 15
 Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
 20 25 30
 Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
 35 40 45
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
 50 55 60
 Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Ala Leu Thr Leu
 65 70 75 80
 Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
 85 90 95
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
 100 105 110
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
 115 120 125
 His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
 130 135 140
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
 145 150 155 160
 Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser Thr
 165 170 175
 His Pro Glu Ser Thr
 180

<210> 67
 <211> 549
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Met IL-29 Pro11 Cys16 mutant Asp170

<221> CDS
 <222> (1)...(549)

<221> variation
 <222> 33, 47, 48
 <223> n = A, T, G, or C

<400> 67
 atg ggc cct gtc ccc act tcc aag ccc acc ccn act ggg aag ggc dnn 48
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Xaa
 1 5 10 15
 cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc 96
 His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
 20 25 30
 aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg 144
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp

35

40

45

agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc 192
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
 50 55 60

cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg 240
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80

ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta 288
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95

gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc 336
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
 100 105 110

tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc 384
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125

cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct 432
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140

ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg 480
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160

cga gac ctc aaa tat gtg gcc gat ggg gay ctg tgt ctg aga acg tca 528
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser
 165 170 175

acc cac cct gag tcc acc tga 549
 Thr His Pro Glu Ser Thr *

<210> 68

<211> 182

<212> PRT

<213> Artificial Sequence

<220>

<223> Met IL-29 Pro11 Cys16 mutant Asp170

<221> VARIANT

<222> (16)...(16)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 68

Met Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Xaa
 1 5 10 15

His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
 20 25 30

Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
 35 40 45

Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
 50 55 60

Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80

Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95

Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala

	100		105		110										
Cys	Ile	Gln	Pro	Gln	Pro	Thr	Ala	Gly	Pro	Arg	Pro	Arg	Gly	Arg	Leu
	115						120					125			
His	His	Trp	Leu	His	Arg	Leu	Gln	Glu	Ala	Pro	Lys	Lys	Glu	Ser	Ala
	130						135				140				
Gly	Cys	Leu	Glu	Ala	Ser	Val	Thr	Phe	Asn	Leu	Phe	Arg	Leu	Leu	Thr
145					150					155					160
Arg	Asp	Leu	Lys	Tyr	Val	Ala	Asp	Gly	Asp	Leu	Cys	Leu	Arg	Thr	Ser
				165			170							175	
Thr	His	Pro	Glu	Ser	Thr										
			180												

<210> 69

<211> 546

<212> DNA

<213> Artificial Sequence

<220>

<223> IL-29 Asp18 Asn169 Cys171 mutant

<221> CDS

<222> (1)...(546)

<221> variation

<222> (512)...(513)

<223> n = A, T, G, or C

<400> 69

ggc	cct	gtc	ccc	act	tcc	aag	ccc	acc	aca	act	ggg	aag	ggc	tgc	cac	48
Gly	Pro	Val	Pro	Thr	Ser	Lys	Pro	Thr	Thr	Thr	Gly	Lys	Gly	Cys	His	
1				5						10				15		

att	gay	agg	ttc	aaa	tct	ctg	tca	cca	cag	gag	cta	gcg	agc	ttc	aag	96
Ile	Asp	Arg	Phe	Lys	Ser	Leu	Ser	Pro	Gln	Glu	Leu	Ala	Ser	Phe	Lys	
			20					25					30			

aag	gcc	agg	gac	gcc	ttg	gaa	gag	tca	ctc	aag	ctg	aaa	aac	tgg	agt	144
Lys	Ala	Arg	Asp	Ala	Leu	Glu	Glu	Ser	Leu	Lys	Leu	Lys	Asn	Trp	Ser	
			35				40					45				

tgc	agc	tct	cct	gtc	ttc	ccc	ggg	aat	tgg	gac	ctg	agg	ctt	ctc	cag	192
Cys	Ser	Ser	Pro	Val	Phe	Pro	Gly	Asn	Trp	Asp	Leu	Arg	Leu	Leu	Gln	
	50					55					60					

gtg	agg	gag	cgc	cct	gtg	gcc	ttg	gag	gct	gag	ctg	gcc	ctg	acg	ctg	240
Val	Arg	Glu	Arg	Pro	Val	Ala	Leu	Glu	Ala	Glu	Leu	Ala	Leu	Thr	Leu	
	65				70				75					80		

aag	gtc	ctg	gag	gcc	gct	gct	ggc	cca	gcc	ctg	gag	gac	gtc	cta	gac	288
Lys	Val	Leu	Glu	Ala	Ala	Ala	Gly	Pro	Ala	Leu	Glu	Asp	Val	Leu	Asp	
				85					90					95		

cag	ccc	ctt	cac	acc	ctg	cac	cac	atc	ctc	tcc	cag	ctc	cag	gcc	tgt	336
Gln	Pro	Leu	His	Thr	Leu	His	His	Ile	Leu	Ser	Gln	Leu	Gln	Ala	Cys	
			100					105					110			

atc	cag	cct	cag	ccc	aca	gca	ggg	ccc	agg	ccc	cgg	ggc	cgc	ctc	cac	384
Ile	Gln	Pro	Gln	Pro	Thr	Ala	Gly	Pro	Arg	Pro	Arg	Gly	Arg	Leu	His	
			115				120					125				

cac	tgg	ctg	cac	cgg	ctc	cag	gag	gcc	ccc	aaa	aag	gag	tcc	gct	ggc	432
His	Trp	Leu	His	Arg	Leu	Gln	Glu	Ala	Pro	Lys	Lys	Glu	Ser	Ala	Gly	
		130				135					140					

tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga 480
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
 145 150 155 160

gac ctc aaa tat gtg gcc gat ggg aac ctg dnn ctg aga acg tca acc 528
 Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr
 165 170 175

cac cct gag tcc acc tga 546
 His Pro Glu Ser Thr *
 180

<210> 70

<211> 181

<212> PRT

<213> Artificial Sequence

<220>

<223> IL-29 Asp18 Asn169 Cys171 mutant

<221> VARIANT

<222> (171)...(171)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 70

Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His
 1 5 10 15
 Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
 20 25 30
 Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
 35 40 45
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
 50 55 60
 Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
 65 70 75 80
 Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
 85 90 95
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
 100 105 110
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
 115 120 125
 His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
 130 135 140
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
 145 150 155 160
 Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr
 165 170 175
 His Pro Glu Ser Thr
 180

<210> 71

<211> 549

<212> DNA

<213> Artificial Sequence

<220>

<223> Met IL-29 Asp19 Asn170 Cys172 mutant

<221> CDS

<222> (1)...(549)

<221> variation

<222> (515)...(516)

<223> n = A, T, G, or C

<400> 71

atg ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc tgc	48
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys	
1 5 10 15	
cac att gay agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc	96
His Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe	
20 25 30	
aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg	144
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp	
35 40 45	
agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc	192
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu	
50 55 60	
cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg	240
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr	
65 70 75 80	
ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta	288
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu	
85 90 95	
gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc	336
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala	
100 105 110	
tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc	384
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu	
115 120 125	
cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct	432
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala	
130 135 140	
ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg	480
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr	
145 150 155 160	
cga gac ctc aaa tat gtg gcc gat ggg aac ctg dnn ctg aga acg tca	528
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser	
165 170 175	
acc cac cct gag tcc acc tga	549
Thr His Pro Glu Ser Thr *	
180	

<210> 72

<211> 182

<212> PRT

<213> Artificial Sequence

<220>

<223> Met IL-29 Asp19 Asn170 Cys172 mutant

<221> VARIANT

<222> (172)...(172)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 72

Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys
 1 5 10 15
 His Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
 20 25 30
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
 35 40 45
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
 50 55 60
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
 100 105 110
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser
 165 170 175
 Thr His Pro Glu Ser Thr
 180

<210> 73

<211> 546

<212> DNA

<213> Artificial Sequence

<220>

<223> IL-29 Cys15 mutant Asp18 Asn169

<221> CDS

<222> (1)...(546)

<221> variation

<222> (44)...(45)

<223> n = A, T, G, or C

<400> 73

ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc dnn cac 48
 Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa His 15
 1 5 10
 att gay agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag 96
 Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys 20 25 30
 aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt 144
 Lys Ala Arg Asp Ala Leu Glu Ser Leu Lys Leu Lys Asn Trp Ser 35 40 45
 tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag 192
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln 50 55 60
 gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg 240
 Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu 65 70 75 80
 aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac 288
 Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp 85 90 95

cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt 336
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
 100 105 110

atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac 384
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
 115 120 125

cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc 432
 His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
 130 135 140

tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga 480
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
 145 150 155 160

gac ctc aaa tat gtg gcc gat ggg aay ctg tgt ctg aga acg tca acc 528
 Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser Thr
 165 170 175

cac cct gag tcc acc tga 546
 His Pro Glu Ser Thr *

<210> 74

<211> 181

<212> PRT

<213> Artificial Sequence

<220>

<223> IL-29 Cys15 mutant Asp18 Asn169

<221> VARIANT

<222> (15)... (15)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 74

Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa His
 1 5 10 15
 Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
 20 25 30
 Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
 35 40 45
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
 50 55 60
 Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
 65 70 75 80
 Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
 85 90 95
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
 100 105 110
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
 115 120 125
 His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
 130 135 140
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
 145 150 155 160
 Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser Thr
 165 170 175
 His Pro Glu Ser Thr
 180

<210> 75
 <211> 549
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Met IL-29 Cys16 mutant Asp19 Asn170

<221> CDS
 <222> (1)...(549)

<221> variation
 <222> (47)...(48)
 <223> n = A, T, G, or C

<400> 75
 atg ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc dnn 48
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa
 1 5 10 15
 cac att gay agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc 96
 His Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
 20 25 30
 aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg 144
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
 35 40 45
 agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc 192
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
 50 55 60
 cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg 240
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta 288
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95
 gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc 336
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
 100 105 110
 tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc 384
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125
 cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct 432
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140
 ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg 480
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160
 cga gac ctc aaa tat gtg gcc gat ggg aay ctg tgt ctg aga acg tca 528
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser
 165 170 175
 acc cac cct gag tcc acc tga 549
 Thr His Pro Glu Ser Thr *
 180

<210> 76
 <211> 182
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Met IL-29 Cys16 mutant Asp19 Asn170

<221> VARIANT
 <222> (16)...(16)
 <223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 76
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa
 1 5 10 15
 His Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
 20 25 30
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
 35 40 45
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
 50 55 60
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
 100 105 110
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser
 165 170 175
 Thr His Pro Glu Ser Thr
 180

<210> 77
 <211> 546
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IL-29 Asp18 Asp169 Cys171 mutant

<221> CDS
 <222> (1)...(546)

<221> variation
 <222> (512)...(513)
 <223> n = A, T, G, or C

<400> 77
 ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc tgc cac 48
 Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His
 1 5 10 15
 att gay agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag 96
 Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
 20 25 30
 aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt 144
 Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser

35	40	45	
tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag	192		
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln			
50 55 60			
gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg	240		
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu			
65 70 75 80			
aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac	288		
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp			
85 90 95			
cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt	336		
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys			
100 105 110			
atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac	384		
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His			
115 120 125			
cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc	432		
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly			
130 135 140			
tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga	480		
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg			
145 150 155 160			
gac ctc aaa tat gtg gcc gat ggg gay ctg dnn ctg aga acg tca acc	528		
Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Xaa Leu Arg Thr Ser Thr			
165 170 175			
cac cct gag tcc acc tga	546		
His Pro Glu Ser Thr *			
180			

<210> 78
 <211> 181
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IL-29 Asp18 Asp169 Cys171 mutant
 <221> VARIANT
 <222> (171)...(171)
 <223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 78
 Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His
 1 5 10 15
 Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
 20 25 30
 Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
 35 40 45
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
 50 55 60
 Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
 65 70 75 80
 Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
 85 90 95
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys

	100		105		110								
Ile	Gln	Pro	Gln	Pro	Thr	Ala	Gly	Pro	Arg	Gly	Arg	Leu	His
	115						120			125			
His	Trp	Leu	His	Arg	Leu	Gln	Glu	Ala	Pro	Lys	Lys	Glu	Ser
	130					135				140			
Cys	Leu	Glu	Ala	Ser	Val	Thr	Phe	Asn	Leu	Phe	Arg	Leu	Leu
	145				150					155			160
Asp	Leu	Lys	Tyr	Val	Ala	Asp	Gly	Asp	Leu	Xaa	Leu	Arg	Thr
				165				170					175
His	Pro	Glu	Ser	Thr									
				180									

<210> 79

<211> 549

<212> DNA

<213> Artificial Sequence

<220>

<223> Met IL-29 Asp19 Asp170 Cys172 mutant

<221> CDS

<222> (1)...(549)

<221> variation

<222> (515)...(516)

<223> n = A, T, G, or C

<400> 79

atg	ggc	cct	gtc	ccc	act	tcc	aag	ccc	acc	aca	act	ggg	aag	ggc	tgc	48
Met	Gly	Pro	Val	Pro	Thr	Ser	Lys	Pro	Thr	Thr	Thr	Gly	Lys	Gly	Cys	
1				5					10					15		

cac	att	gay	agg	ttc	aaa	tct	ctg	tca	cca	cag	gag	cta	gcg	agc	ttc	96
His	Ile	Asp	Arg	Phe	Lys	Ser	Leu	Ser	Pro	Gln	Glu	Leu	Ala	Ser	Phe	
			20					25				30				

aag	aag	gcc	agg	gac	gcc	ttg	gaa	gag	tca	ctc	aag	ctg	aaa	aac	tgg	144
Lys	Lys	Ala	Arg	Asp	Ala	Leu	Glu	Glu	Ser	Leu	Lys	Leu	Lys	Asn	Trp	
		35				40						45				

agt	tgc	agc	tct	cct	gtc	ttc	ccc	ggg	aat	tgg	gac	ctg	agg	ctt	ctc	192
Ser	Cys	Ser	Ser	Pro	Val	Phe	Pro	Gly	Asn	Trp	Asp	Leu	Arg	Leu	Leu	
	50					55					60					

cag	gtg	agg	gag	cgc	cct	gtg	gcc	ttg	gag	gct	gag	ctg	gcc	ctg	acg	240
Gln	Val	Arg	Glu	Arg	Pro	Val	Ala	Leu	Glu	Ala	Glu	Leu	Ala	Leu	Thr	
	65				70				75						80	

ctg	aag	gtc	ctg	gag	gcc	gct	gct	ggc	cca	gcc	ctg	gag	gac	gtc	cta	288
Leu	Lys	Val	Leu	Glu	Ala	Ala	Ala	Gly	Pro	Ala	Leu	Glu	Asp	Val	Leu	
			85					90						95		

gac	cag	ccc	ctt	cac	acc	ctg	cac	cac	atc	ctc	tcc	cag	ctc	cag	gcc	336
Asp	Gln	Pro	Leu	His	Thr	Leu	His	His	Ile	Leu	Ser	Gln	Leu	Gln	Ala	
			100					105					110			

tgt	atc	cag	cct	cag	ccc	aca	gca	ggg	ccc	agg	ccc	cgg	ggc	cgc	ctc	384
Cys	Ile	Gln	Pro	Gln	Pro	Thr	Ala	Gly	Pro	Arg	Pro	Arg	Gly	Arg	Leu	
		115					120					125				

cac	cac	tgg	ctg	cac	cgg	ctc	cag	gag	gcc	ccc	aaa	aag	gag	tcc	gct	432
His	His	Trp	Leu	His	Arg	Leu	Gln	Glu	Ala	Pro	Lys	Lys	Glu	Ser	Ala	
		130				135					140					

ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg 480
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160

cga gac ctc aaa tat gtg gcc gat ggg gay ctg dnn ctg aga acg tca 528
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Xaa Leu Arg Thr Ser
 165 170 175

acc cac cct gag tcc acc tga 549
 Thr His Pro Glu Ser Thr *
 180

<210> 80
 <211> 182
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Met IL-29 Asp19 Asp170 Cys172 mutant

<221> VARIANT
 <222> (172)...(172)
 <223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 80
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys
 1 5 10 15
 His Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
 20 25 30
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
 35 40 45
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
 50 55 60
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
 100 105 110
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Xaa Leu Arg Thr Ser
 165 170 175
 Thr His Pro Glu Ser Thr
 180

<210> 81
 <211> 546
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IL-29 Cys15 mutant Asp18 Asp169

<221> CDS
 <222> (1)...(546)
 <221> variation
 <222> (44)...(45)

<223> n = A, T, G, or C

<400> 81
 ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc dnn cac 48
 Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa His
 1 5 10 15
 att gay agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag 96
 Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
 20 25 30
 aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt 144
 Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
 35 40 45
 tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag 192
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
 50 55 60
 gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg 240
 Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
 65 70 75 80
 aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac 288
 Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
 85 90 95
 cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt 336
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
 100 105 110
 atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac 384
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
 115 120 125
 cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc 432
 His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
 130 135 140
 tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga 480
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
 145 150 155 160
 gac ctc aaa tat gtg gcc gat ggg gay ctg tgt ctg aga acg tca acc 528
 Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser Thr
 165 170 175
 cac cct gag tcc acc tga 546
 His Pro Glu Ser Thr *

<210> 82
 <211> 181
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IL-29 Cys15 mutant Asp18 Asp169
 <221> VARIANT
 <222> (15)...(15)
 <223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 82

Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa His
 1 5 10 15
 Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
 20 25 30
 Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
 35 40 45
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
 50 55 60
 Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
 65 70 75 80
 Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
 85 90 95
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
 100 105 110
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
 115 120 125
 His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
 130 135 140
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
 145 150 155 160
 Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser Thr
 165 170 175
 His Pro Glu Ser Thr
 180

<210> 83
 <211> 549
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Met IL-29 Cys16 mutant Asp19 Asp170

<221> CDS
 <222> (1)...(549)

<221> variation
 <222> (47)...(48)
 <223> n = A, T, G, or C

<400> 83
 atg ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc dnn 48
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa
 1 5 10 15
 cac att gay agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc 96
 His Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
 20 25 30
 aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg 144
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
 35 40 45
 agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc 192
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
 50 55 60
 cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg 240
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta 288
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95

gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc 336
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
 100 105 110

tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc 384
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125

cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct 432
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140

ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg 480
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160

cga gac ctc aaa tat gtg gcc gat ggg gay ctg tgt ctg aga acg tca 528
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser
 165 170 175

acc cac cct gag tcc acc tga 549
 Thr His Pro Glu Ser Thr *

<210> 84
 <211> 182
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Met IL-29 Cys16 mutant Asp19 Asp170

<221> VARIANT
 <222> (16)...(16)
 <223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 84
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa
 1 5 10 15
 His Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
 20 25 30
 Lys Lys Ala Arg Asp Ala Leu Glu Ser Leu Lys Leu Lys Asn Trp
 35 40 45
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
 50 55 60
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
 100 105 110
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser
 165 170 175
 Thr His Pro Glu Ser Thr
 180

<210> 85
 <211> 528
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IL-28B Cys48 mutant

<221> CDS
 <222> (1)...(528)

<221> variation
 <222> (143)...(144)
 <223> n = A, T, G, or C

<400> 85
 gtt cct gtc gcc agg ctc cgc ggg gct ctc ccg gat gca agg ggc tgc 48
 Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly Cys 15
 1 5 10
 cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc ttt 96
 His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe 30
 20 25
 aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac dnn 144
 Lys Arg Ala Lys Asp Ala Leu Glu Ser Leu Leu Leu Lys Asp Xaa 45
 35 40
 aag tgc cgc tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag ctg 192
 Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu 60
 50 55
 cag gtg agg gag cgc ccc gtg gct ttg gag gct gag ctg gcc ctg acg 240
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr 80
 65 70 75
 ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg ggg gat 288
 Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Gly Asp 95
 85 90
 gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag ctc 336
 Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu 110
 100 105
 cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg ggc 384
 Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly 125
 115 120
 cgc ctc cac cat tgg ctg cac cgg ctc cag gag gcc cca aaa aag gag 432
 Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu 140
 130 135
 tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc ctc 480
 Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu 160
 145 150 155
 ctc acg cga gac ctg aat tgt gtt gcc agc ggg gac ctg tgt gtc tga 528
 Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val * 175
 165 170

<210> 86
 <211> 175
 <212> PRT

<213> Artificial Sequence

<220>

<223> IL-28B Cys48 mutant

<221> VARIANT

<222> (48)...(48)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 86

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Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly Cys
1      5      10      15
His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe
20      25      30
Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp Xaa
35      40      45
Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu
50      55      60
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
65      70      75      80
Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Gly Asp
85      90      95
Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu
100     105     110
Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly
115     120     125
Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu
130     135     140
Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
145     150     155     160
Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
165     170     175

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<210> 87

<211> 531

<212> DNA

<213> Artificial Sequence

<220>

<223> Met IL-28B Cys49 mutant

<221> CDS

<222> (1)...(531)

<221> variation

<222> (146)...(147)

<223> n = A, T, G, or C

<400> 87

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atg gtt cct gtc gcc agg ctc cgc ggg gct ctc ccg gat gca agg ggc 48
Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
1      5      10      15

tgc cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc 96
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
20      25      30

ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac 144
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
35      40      45

dnn aag tgc cgc tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag 192
Xaa Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
50      55      60

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ctg cag gtg agg gag cgc ccc gtg gct ttg gag gct gag ctg gcc ctg 240
 Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
 65 70 75 80

acg ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg ggg 288
 Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Gly
 85 90 95

gat gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag 336
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
 100 105 110

ctc cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg 384
 Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
 115 120 125

ggc cgc ctc cac cat tgg ctg cac cgg ctc cag gag gcc cca aaa aag 432
 Gly Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys
 130 135 140

gag tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc 480
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
 145 150 155 160

ctc ctc acg cga gac ctg aat tgt gtt gcc agc ggg gac ctg tgt gtc 528
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175

tga 531
 *

<210> 88

<211> 176

<212> PRT

<213> Artificial Sequence

<220>

<223> Met IL-28B Cys49 mutant

<221> VARIANT

<222> (49)...(49)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 88

Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
 1 5 10 15
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
 20 25 30
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp
 35 40 45
 Xaa Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
 50 55 60
 Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
 65 70 75 80
 Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Gly
 85 90 95
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
 100 105 110
 Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
 115 120 125
 Gly Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys
 130 135 140

Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
 145 150 155 160
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175

<210> 89
 <211> 528
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IL-28B Cys50 mutant

<221> CDS
 <222> (1)...(528)

<221> variation
 <222> (149)...(150)
 <223> n = A, T, G, or C

<400> 89
 gtt cct gtc gcc agg ctc cgc ggg gct ctc ccg gat gca agg ggc tgc 48
 Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly Cys
 1 5 10 15
 cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc ttt 96
 His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe
 20 25 30
 aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac tgc 144
 Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp Cys
 35 40 45
 aag dnn cgc tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag ctg 192
 Lys Xaa Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu
 50 55 60
 cag gtg agg gag cgc ccc gtg gct ttg gag gct gag ctg gcc ctg acg 240
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg ggg gat 288
 Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Gly Asp
 85 90 95
 gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag ctc 336
 Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu
 100 105 110
 cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg ggc 384
 Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly
 115 120 125
 cgc ctc cac cat tgg ctg cac cgg ctc cag gag gcc cca aaa aag gag 432
 Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu
 130 135 140
 tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc ctc 480
 Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
 145 150 155 160
 ctc acg cga gac ctg aat tgt gtt gcc agc ggg gac ctg tgt gtc tga 528
 Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val *
 165 170 175

<210> 90
 <211> 175
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IL-28B Cys50 mutant

<221> VARIANT
 <222> (50)...(50)
 <223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 90
 Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly Cys
 1 5 10 15
 His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe
 20 25 30
 Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp Cys
 35 40 45
 Lys Xaa Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu
 50 55 60
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Gly Asp
 85 90 95
 Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu
 100 105 110
 Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly
 115 120 125
 Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu
 130 135 140
 Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
 145 150 155 160
 Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175

<210> 91
 <211> 531
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Met IL-28B Cys51 mutant

<221> CDS
 <222> (1)...(531)

<221> variation
 <222> (152)...(153)
 <223> n = A, T, G, or C

<400> 91
 atg gtt cct gtc gcc agg ctc cgc ggg gct ctc ccg gat gca agg ggc 48
 Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly 15
 1 5 10
 tgc cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc 96
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala 30
 20 25
 ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac 144

Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
 35 40 45
 tgc aag dnn cgc tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag 192
 Cys Lys Xaa Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
 50 55 60
 ctg cag gtg agg gag cgc ccc gtg gct ttg gag gct gag ctg gcc ctg 240
 Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
 65 70 75 80
 acg ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg ggg 288
 Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Gly
 85 90 95
 gat gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag 336
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
 100 105 110
 ctc cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg 384
 Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
 115 120 125
 ggc cgc ctc cac cat tgg ctg cac cgg ctc cag gag gcc cca aaa aag 432
 Gly Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys
 130 135 140
 gag tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc 480
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
 145 150 155 160
 ctc ctc acg cga gac ctg aat tgt gtt gcc agc ggg gac ctg tgt gtc 528
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175
 tga 531
 *

<210> 92
 <211> 176
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Met IL-28B Cys51 mutant
 <221> VARIANT
 <222> (51)...(51)
 <223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 92
 Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
 1 5 10 15
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
 20 25 30
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp
 35 40 45
 Cys Lys Xaa Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
 50 55 60
 Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
 65 70 75 80
 Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Gly
 85 90 95

Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
 100 105 110
 Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
 115 120 125
 Gly Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys
 130 135 140
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
 145 150 155 160
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175

<210> 93
 <211> 528
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IL-28B Cys48 mutant T87S H135Y

<221> CDS
 <222> (1)...(528)

<221> variation
 <222> 143, 144, 261
 <223> n = A, T, G, or C

<400> 93
 gtt cct gtc gcc agg ctc cgc ggg gct ctc ccg gat gca agg ggc tgc 48
 Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly Cys
 1 5 10 15
 cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc ttt 96
 His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe
 20 25 30
 aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac dnn 144
 Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp Xaa
 35 40 45
 aag tgc cgc tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag ctg 192
 Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu
 50 55 60
 cag gtg agg gag cgc ccc gtg gct ttg gag gct gag ctg gcc ctg acg 240
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 ctg aag gtt ctg gag gcc wsn gct gac act gac cca gcc ctg ggg gat 288
 Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly Asp
 85 90 95
 gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag ctc 336
 Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu
 100 105 110
 cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg ggc 384
 Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly
 115 120 125
 cgc ctc cac cat tgg ctg tay cgg ctc cag gag gcc cca aaa aag gag 432
 Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu
 130 135 140
 tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc ctc 480

Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
 145 150 155 160
 ctc acg cga gac ctg aat tgt gtt gcc agc ggg gac ctg tgt gtc tga 528
 Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val *
 165 170 175

<210> 94
 <211> 175
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> VARIANT
 <222> (48)...(48)
 <223> Xaa = Ser, Ala, Thr, Val, or Asn

<221> VARIANT
 <222> (87)...(87)
 <223> Xaa = Ser

<223> IL-28B Cys48 mutant T87S H135Y

<400> 94
 Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly Cys
 1 5 10 15
 His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe
 20 25 30
 Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp Xaa
 35 40 45
 Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu
 50 55 60
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly Asp
 85 90 95
 Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu
 100 105 110
 Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly
 115 120 125
 Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu
 130 135 140
 Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
 145 150 155 160
 Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175

<210> 95
 <211> 531
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Met IL-28B Cys49 mutant T88S H136Y

<221> CDS
 <222> (1)...(531)

<221> variation
 <222> 146, 147, 264
 <223> n = A, T, G, or C

<400> 95
 atg gtt cct gtc gcc agg ctc cgc ggg gct ctc ccg gat gca agg ggc 48
 Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
 1 5 10 15

 tgc cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc 96
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
 20 25 30

 ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac 144
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
 35 40 45

 dnn aag tgc cgc tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag 192
 Xaa Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
 50 55 60

 ctg cag gtg agg gag cgc ccc gtg gct ttg gag gct gag ctg gcc ctg 240
 Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
 65 70 75 80

 acg ctg aag gtt ctg gag gcc wsn gct gac act gac cca gcc ctg ggg 288
 Thr Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly
 85 90 95

 gat gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag 336
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
 100 105 110

 ctc cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg 384
 Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
 115 120 125

 ggc cgc ctc cac cat tgg ctg tay cgg ctc cag gag gcc cca aaa aag 432
 Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
 130 135 140

 gag tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc 480
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
 145 150 155 160

 ctc ctc acg cga gac ctg aat tgt gtt gcc agc ggg gac ctg tgt gtc 528
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175

 tga 531
 *

<210> 96
 <211> 176
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> VARIANT
 <222> (49)...(49)
 <223> Xaa = Ser, Ala, Thr, Val, or Asn

<221> VARIANT
 <222> (136)...(136)
 <223> Xaa = Ser

 <223> Met IL-28B Cys49 mutant T88S H136Y

<400> 96
 Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
 1 5 10 15
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
 20 25 30
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
 35 40 45
 Xaa Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
 50 55 60
 Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
 65 70 75 80
 Thr Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly
 85 90 95
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
 100 105 110
 Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
 115 120 125
 Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
 130 135 140
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
 145 150 155 160
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175

<210> 97
 <211> 528
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IL-28B Cys50 mutant T87S H135Y

<221> CDS
 <222> (1)...(528)

<221> variation
 <222> 149, 150, 261
 <223> n = A, T, G, or C

<400> 97
 gtt cct gtc gcc agg ctc cgc ggg gct ctc ccg gat gca agg ggc tgc 48
 Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly Cys
 1 5 10 15
 cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc ttt 96
 His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe
 20 25 30
 aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac tgc 144
 Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp Cys
 35 40 45
 aag dnn cgc tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag ctg 192
 Lys Xaa Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu
 50 55 60
 cag gtg agg gag cgc ccc gtg gct ttg gag gct gag ctg gcc ctg acg 240
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 ctg aag gtt ctg gag gcc wsn gct gac act gac cca gcc ctg ggg gat 288
 Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly Asp
 85 90 95

gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag ctc 336
 Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu
 100 105 110

cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg ggc 384
 Arg Ala Cys Ile Gln Pro Gln Thr Ala Gly Pro Arg Thr Arg Gly
 115 120 125

cgc ctc cac cat tgg ctg tay cgg ctc cag gag gcc cca aaa aag gag 432
 Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu
 130 135 140

tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc ctc 480
 Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
 145 150 155 160

ctc acg cga gac ctg aat tgt gtt gcc agc ggg gac ctg tgt gtc tga 528
 Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val *
 165 170 175

<210> 98
 <211> 175
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> VARIANT
 <222> (50)...(50)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<221> VARIANT
 <222> (87)...(87)
 <223> Xaa = Ser

<223> IL-28B Cys50 mutant T87S H135Y

<400> 98
 Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly Cys
 1 5 10 15
 His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe
 20 25 30
 Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp Cys
 35 40 45
 Lys Xaa Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu
 50 55 60
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly Asp
 85 90 95
 Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu
 100 105 110
 Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly
 115 120 125
 Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu
 130 135 140
 Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
 145 150 155 160
 Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175

<210> 99

<211> 531
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Met IL-28B Cys51 mutant T88S H136Y

<221> CDS
 <222> (1)...(531)

<221> variation
 <222> 152, 152, 264
 <223> n = A, T, G, or C

<400> 99
 atg gtt cct gtc gcc agg ctc cgc ggg gct ctc ccg gat gca agg ggc 48
 Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
 1 5 10 15

tgc cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc 96
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
 20 25 30

ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac 144
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
 35 40 45

tgc aag dnn cgc tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag 192
 Cys Lys Xaa Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
 50 55 60

ctg cag gtg agg gag cgc ccc gtg gct ttg gag gct gag ctg gcc ctg 240
 Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
 65 70 75 80

acg ctg aag gtt ctg gag gcc wsn gct gac act gac cca gcc ctg ggg 288
 Thr Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly
 85 90 95

gat gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag 336
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
 100 105 110

ctc cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg 384
 Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
 115 120 125

ggc cgc ctc cac cat tgg ctg tay cgg ctc cag gag gcc cca aaa aag 432
 Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
 130 135 140

gag tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc 480
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
 145 150 155 160

ctc ctc acg cga gac ctg aat tgt gtt gcc agc ggg gac ctg tgt gtc 528
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175

tga
 *

531

<211> 176
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> VARIANT
 <222> (51)...(51)
 <223> Xaa = Ser, Ala, Thr, Val, or Asn

<221> VARIANT
 <222> (88)...(88)
 <223> Xaa = Ser

<223> Met IL-28B Cys51 mutant T88S H136Y

<400> 100
 Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
 1 5 10 15
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
 20 25 30
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
 35 40 45
 Cys Lys Xaa Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
 50 55 60
 Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
 65 70 75 80
 Thr Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly
 85 90 95
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
 100 105 110
 Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
 115 120 125
 Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
 130 135 140
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
 145 150 155 160
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175

<210> 101
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> signal sequence

<221> CDS
 <222> (1)...(45)

<221> variation
 <222> 6, 9, 12, 18, 21, 24, 27, 30, 33, 36, 39, 42, 45
 <223> n = A, T, G, or C

<400> 101
 atg gcn gcn gcn tgg acn gtn gtn ytn gtn acn ytn gtn ytn ggn 45
 Met Ala Ala Ala Trp Thr Val Val Leu Val Thr Leu Val Leu Gly
 1 5 10 15

<210> 102
 <211> 15
 <212> PRT

<213> Artificial Sequence

<220>

<223> signal sequence

<400> 102

Met Ala Ala Ala Trp Thr Val Val Leu Val Thr Leu Val Leu Gly
 1 5 10 15

<210> 103

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> signal sequence

<221> CDS

<222> (1)...(57)

<221> variation

<222> 6, 9, 12, 18, 21, 24, 27, 30, 33, 36, 39, 42, 45, 48, 51,
 54, 57

<223> n = A, T, G, or C

<400> 103

atg gcn gcn gcn tgg acn gtn gtn ytn gtn acn ytn gtn ytn ggn ytn 48
 Met Ala Ala Ala Trp Thr Val Val Leu Val Thr Leu Val Leu Gly Leu
 1 5 10 15

gcn gtn gcn 57
 Ala Val Ala

<210> 104

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> signal sequence

<400> 104

Met Ala Ala Ala Trp Thr Val Val Leu Val Thr Leu Val Leu Gly Leu
 1 5 10 15
 Ala Val Ala

<210> 105

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> signal sequence

<221> CDS

<222> (1)...(63)

<221> variation

<222> 6, 9, 12, 18, 21, 24, 27, 30, 33, 36, 39, 42, 45, 48, 51,
 54, 57, 60, 63

<223> n = A, T, G, or C

<400> 105
 atg gcn gcn gcn tgg acn gtn gtn ytn gtn acn ytn gtn ytn ggn ytn 48
 Met Ala Ala Ala Trp Thr Val Val Leu Val Thr Leu Val Leu Gly Leu
 1 5 10 15
 gcn gtn gcn ggn ccn 63
 Ala Val Ala Gly Pro
 20

<210> 106
 <211> 21
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> signal sequence

<400> 106
 Met Ala Ala Ala Trp Thr Val Val Leu Val Thr Leu Val Leu Gly Leu
 1 5 10 15
 Ala Val Ala Gly Pro
 20

<210> 107
 <211> 72
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> signal sequence

<221> CDS
 <222> (1)...(72)

<221> variation
 <222> 6, 9, 12, 18, 21, 24, 27, 30, 33, 36, 39, 42, 45, 48, 51,
 54, 57, 60, 63, 66, 69, 72
 <223> n = A, T, G, or C

<400> 107
 atg gcn gcn gcn tgg acn gtn gtn ytn gtn acn ytn gtn ytn ggn ytn 48
 Met Ala Ala Ala Trp Thr Val Val Leu Val Thr Leu Val Leu Gly Leu
 1 5 10 15
 gcn gtn gcn ggn ccn gtn ccn acn 72
 Ala Val Ala Gly Pro Val Pro Thr
 20

<210> 108
 <211> 24
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> signal sequence

<400> 108
 Met Ala Ala Ala Trp Thr Val Val Leu Val Thr Leu Val Leu Gly Leu
 1 5 10 15
 Ala Val Ala Gly Pro Val Pro Thr

20

<210> 109
 <211> 546
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IL-29 C171X

<221> CDS
 <222> (1)...(546)

<221> variation
 <222> (512)...(513)
 <223> n = A, T, G, or C

<400> 109
 ggt ccg gtt ceg acc tct aaa cca acc acc act ggt aaa ggt tgc cac 48
 Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His
 1 5 10 15
 atc ggt cgt ttc aaa tct ctg tct ccg cag gaa ctg gct tct ttc aaa 96
 Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
 20 25 30
 aaa gct cgt gac gct ctg gaa gaa tct ctg aaa ctg aaa aac tgg tct 144
 Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
 35 40 45
 tgc tct tct ccg gtt ttc ccg ggt aac tgg gat ctg cgt ctg ctg cag 192
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
 50 55 60
 gtt cgt gaa cgt ccg gtt gct ctg gaa gct gaa ctg gct ctg acc ctg 240
 Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
 65 70 75 80
 aaa gtt ctg gaa gct gct gca ggt cct gct ctg gaa gat gtt ctg gat 288
 Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
 85 90 95
 cag ccg ctg cac act ctg cac cac atc ctg tct cag ctg cag gct tgc 336
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
 100 105 110
 att caa ccg caa ccg acc gct ggt ccg cgt ccg cgt ggt cgt ctg cac 384
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
 115 120 125
 cac tgg ctg cat cgt ctg cag gaa gct ccg aaa aaa gaa tct gct ggt 432
 His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
 130 135 140
 tgc ctg gaa gct tct gtt acc ttc aac ctg ttc cgt ctg ctg acc cgt 480
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
 145 150 155 160
 gat ctg aaa tac gtt gct gat ggt aac ctg dnn ctg cgt acc tct acc 528
 Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr
 165 170 175
 cat ccg gaa tct acc taa 546
 His Pro Glu Ser Thr *

180

<210> 110
 <211> 181
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IL-29 C171X

<221> VARIANT
 <222> (171)...(171)
 <223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 110
 Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His
 1 5 10 15
 Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
 20 25 30
 Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
 35 40 45
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
 50 55 60
 Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
 65 70 75 80
 Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
 85 90 95
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
 100 105 110
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
 115 120 125
 His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
 130 135 140
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
 145 150 155 160
 Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr
 165 170 175
 His Pro Glu Ser Thr
 180

<210> 111
 <211> 549
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Met IL-29 C172X

<221> CDS
 <222> (1)...(549)

<221> variation
 <222> (515)...(516)
 <223> n = A, T, G, or C

<400> 111
 atg ggt ccg gtt ccg acc tct aaa cca acc acc act ggt aaa ggt tgc 48
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys
 1 5 10 15
 cac atc ggt cgt ttc aaa tct ctg tct ccg cag gaa ctg gct tct ttc 96
 His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
 20 25 30

aaa aaa gct cgt gac gct ctg gaa gaa tct ctg aaa ctg aaa aac tgg 144
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
35 40 45

tct tgc tct tct ccg gtt ttc ccg ggt aac tgg gat ctg cgt ctg ctg 192
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
50 55 60

cag gtt cgt gaa cgt ccg gtt gct ctg gaa gct gaa ctg gct ctg acc 240
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
65 70 75 80

ctg aaa gtt ctg gaa gct gct gca ggt cct gct ctg gaa gat gtt ctg 288
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
85 90 95

gat cag ccg ctg cac act ctg cac cac atc ctg tct cag ctg cag gct 336
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
100 105 110

tgc att caa ccg caa ccg acc gct ggt ccg cgt ccg cgt ggt cgt ctg 384
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
115 120 125

cac cac tgg ctg cat cgt ctg cag gaa gct ccg aaa aaa gaa tct gct 432
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
130 135 140

ggt tgc ctg gaa gct tct gtt acc ttc aac ctg ttc cgt ctg ctg acc 48
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
1-45 150 155 160

cgt gat ctg aaa tac gtt gct gat ggt aac ctg dnn ctg cgt acc tct 52
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser
165 170 175

acc cat ccg gaa tct acc taa
Thr His Pro Glu Ser Thr *

```
<210> 112
<211> 182
<212> PRT
<213> Artificial Sequence
```

<220>
<223> Met IL-29 C172X

```
<221> VARIANT
<222> (172)...(172)
<223> Xaa = Ser, Ala, Thr, Val, or Asn
```

<400> 112															
Met	Gly	Pro	Val	Pro	Thr	Ser	Lys	Pro	Thr	Thr	Thr	Gly	Lys	Gly	Cys
1				5					10					15	
His	Ile	Gly	Arg	Phe	Lys	Ser	Leu	Ser	Pro	Gln	Glu	Leu	Ala	Ser	Phe
			20					25					30		
Lys	Lys	Ala	Arg	Asp	Ala	Leu	Glu	Glu	Ser	Leu	Lys	Leu	Lys	Asn	Trp
		35				40						45			
Ser	Cys	Ser	Ser	Pro	Val	Phe	Pro	Gly	Asn	Trp	Asp	Leu	Arg	Leu	Leu
	50					55					60				
Gln	Val	Arg	Glu	Arg	Pro	Val	Ala	Leu	Glu	Ala	Glu	Leu	Ala	Leu	Thr
65					70					75					80

Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
 100 105 110
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser
 165 170 175
 Thr His Pro Glu Ser Thr
 180

<210> 113

<211> 543

<212> DNA

<213> Artificial Sequence

<220>

<223> IL-29 C170X, truncated after N-terminal Methionine
and Glycine

<221> CDS

<222> (1)...(543)

<221> variation

<222> (509)...(510)

<223> n = A, T, G, or C

<400> 113

cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc tgc cac att 48
 Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile
 1 5 10 15
 ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag aag 96
 Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys
 20 25 30
 gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt tgc 144
 Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys
 35 40 45
 agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag gtg 192
 Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val
 50 55 60
 agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg aag 240
 Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys
 65 70 75 80
 gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac cag 288
 Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln
 85 90 95
 ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt atc 336
 Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile
 100 105 110
 cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac cac 384
 Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His
 115 120 125

```

tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc tgc      432
Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys
   130                      135                      140

ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga gac      480
Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp
   145                      150                      155                      160

ctc aaa tat gtg gcc gat ggg aac ctg dnn ctg aga acg tca acc cac      528
Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His
           165                      170                      175

cct gag tcc acc tga      543
Pro Glu Ser Thr *
           180

```

```

<210> 114
<211> 180
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> IL-29 C170X, truncated after N-terminal Methionine
      and Glycine

```

```

<221> VARIANT
<222> (170)...(170)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

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```

<400> 114
Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile
 1          5          10          15
Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys
 20          25          30
Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys
 35          40          45
Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val
 50          55          60
Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys
 65          70          75          80
Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln
 85          90          95
Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile
 100         105         110
Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His
 115         120         125
Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys
 130         135         140
Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp
 145         150         155         160
Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His
 165         170         175

Pro Glu Ser Thr
           180

```

```

<210> 115
<211> 540
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> IL-29 C169X, truncated after N-terminal

```

Methionine, Glycine, and Proline

<221> CDS

<222> (1)...(540)

<221> variation

<222> (506)...(507)

<223> n = A, T, G, or C

<400> 115

gtc ccc act tcc aag ccc acc aca act ggg aag ggc tgc cac att ggc 48
 Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly 15

agg ttc aaa tct ctg tca cca cag gag cta ggc agc ttc aag aag gcc 96
 Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala 30
 20 25

agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt tgc agc 144
 Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser 45
 35 40

tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag gtg agg 192
 Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg 60
 50 55

gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg aag gtc 240
 Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val 80
 65 70 75

ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac cag ccc 288
 Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro 95
 85 90

ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt atc cag 336
 Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln 110
 100 105

cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac cac tgg 384
 Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp 125
 115 120

ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc tgc ctg 432
 Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu 140
 130 135

gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga gac ctc 480
 Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu 160
 145 150 155

aaa tat gtg gcc gat ggg aac ctg dnn ctg aga acg tca acc cac cct 528
 Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro 175
 165 170

gag tcc acc tga 540
 Glu Ser Thr *

<210> 116

<211> 179

<212> PRT

<213> Artificial Sequence

<220>

<223> IL-29 C169X, truncated after N-terminal
Methionine, Glycine, and Proline

<221> VARIANT

<222> (169)....(169)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 116
Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly
1 5 10 15
Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala
20 25 30
Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser
35 40 45
Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg
50 55 60
Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val
65 70 75 80
Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro
85 90 95
Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln
100 105 110
Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp
115 120 125
Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu
130 135 140
Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu
145 150 155 160
Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro
165 170 175
Glu Ser Thr

<210> 117

<211> 537

<212> DNA

<213> Artificial Sequence

<220>

<223> IL-29 C168X, truncated after N-terminal
Methionine, Glycine, Proline, and Valine

<221> CDS

<222> (1)...(537)

<221> variation

<222> (503)...(504)

<223> n = A, T, G, or C

<400> 117
ccc act tcc aag ccc acc aca act ggg aag ggc tgc cac att ggc agg 48
Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly Arg
1 5 10 15
ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag aag gcc agg 96
Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg
20 25 30
gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt tgc agc tct 144
Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser
35 40 45
cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag gtg agg gag 192
Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu

50 55 60 240
 cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg aag gtc ctg
 Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu
 65 70 75 80
 gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac cag ccc ctt 288
 Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu
 85 90 95
 cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt atc cag cct 336
 His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro
 100 105 110
 cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac cac tgg ctg 384
 Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu
 115 120 125
 cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc tgc ctg gag 432
 His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu
 130 135 140
 gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga gac ctc aaa 480
 Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys
 145 150 155 160
 tat gtg gcc gat ggg aac ctg dnn ctg aga acg tca acc cac cct gag 528
 Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro Glu
 165 170 175
 tcc acc tga 537
 Ser Thr *

<210> 118
 <211> 178
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IL-29 C168X, truncated after N-terminal
 Methionine, Glycine, Proline, and Valine

<221> VARIANT
 <222> (168)...(168)
 <223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 118
 Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly Arg
 1 5 10 15
 Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg
 20 25 30
 Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser
 35 40 45
 Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu
 50 55 60
 Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu
 65 70 75 80
 Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu
 85 90 95
 His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro
 100 105 110
 Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu
 115 120 125

His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu
 130 135 140
 Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys
 145 150 155 160
 Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro Glu
 165 170 175
 Ser Thr

<210> 119

<211> 534

<212> DNA

<213> Artificial Sequence

<220>

<223> IL-29 C167X, truncated after N-terminal
 Methionine, Glycine, Proline, Valine, and Proline

<221> CDS

<222> (1)...(534)

<221> variation

<222> (500)...(501)

<223> n = A, T, G, or C

<400> 119

act tcc aag ccc acc aca act ggg aag ggc tgc cac att ggc agg ttc 48
 Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly Arg Phe
 1 5 10 15

aaa tct ctg tca cca cag gag cta gcg agc ttc aag aag gcc agg gac 96
 Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg Asp
 20 25 30

gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt tgc agc tct cct 144
 Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser Pro
 35 40 45

gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag gtg agg gag cgc 192
 Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu Arg
 50 55 60

cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg aag gtc ctg gag 240
 Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu
 65 70 75 80

gcc gct gct ggc cca gcc ctg gag gac gtc cta gac cag ccc ctt cac 288
 Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu His
 85 90 95

acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt atc cag cct cag 336
 Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro Gln
 100 105 110

ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac cac tgg ctg cac 384
 Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu His
 115 120 125

cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc tgc ctg gag gca 432
 Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu Ala
 130 135 140

tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga gac ctc aaa tat 480
 Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys Tyr

145	150	155	160	
gtg gcc gat ggg aac ctg dnn ctg aga acg tca acc cac cct gag tcc				528
Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro Glu Ser				
	165	170	175	
acc tga				534
Thr *				

```
<210> 120
<211> 177
<212> PRT
<213> Artificial Sequence
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<220>
<223> IL-29 C167X, truncated after N-terminal
Methionine, Glycine, Proline, Valine, and Proline

```
<221> VARIANT
<222> (167)...(167)
<223> Xaa = Ser, Ala, Thr, Val, or Asn
```

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524
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<210> 121
<211> 531
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-29 C166X, truncated after N-terminal
Methionine, Glycine, Proline, Valine, Proline, and
Threonine

```
<221> CDS
<222> (1)...(531)
<221> variation
```

<222> (497)...(498)

<223> n = A, T, G, or C

<400> 121

tcc aag ccc acc aca act ggg aag ggc tgc cac att ggc agg ttc aaa 48
 Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly Arg Phe Lys 15
 1 5 10

tct ctg tca cca cag gag cta ggc agc ttc aag aag gcc agg gac gcc 96
 Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg Asp Ala 30
 20 25

ttg gaa gag tca ctc aag ctg aaa aac tgg agt tgc agc tct cct gtc 144
 Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser Pro Val 45
 35 40

ttc ccc ggg aat tgg gac ctg agg ctt ctc cag gtg agg gag cgc cct 192
 Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu Arg Pro 60
 50 55

gtg gcc ttg gag gct gag ctg gcc ctg acg ctg aag gtc ctg gag gcc 240
 Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala 80
 65 70 75

gct gct ggc cca gcc ctg gag gac gtc cta gac cag ccc ctt cac acc 288
 Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu His Thr 95
 85 90

ctg cac cac atc ctc tcc cag ctc cag gcc tgt atc cag cct cag ccc 336
 Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro Gln Pro 110
 100 105

aca gca ggg ccc agg ccc cgg ggc cgc ctc cac cac tgg ctg cac cgg 384
 Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu His Arg 125
 115 120

ctc cag gag gcc ccc aaa aag gag tcc gct ggc tgc ctg gag gca tct 432
 Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu Ala Ser 140
 130 135

gtc acc ttc aac ctc ttc cgc ctc ctc acg cga gac ctc aaa tat gtg 480
 Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys Tyr Val 160
 145 150 155

gcc gat ggg aac ctg dnn ctg aga acg tca acc cac cct gag tcc acc 528
 Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro Glu Ser Thr 175
 165 170

531

tga

*

<210> 122

<211> 176

<212> PRT

<213> Artificial Sequence

<220>

<223> IL-29 C166X, truncated after N-terminal
 Methionine, Glycine, Proline, Valine, Proline, and
 Threonine

<221> VARIANT

<222> (166)...(166)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 122
 Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly Arg Phe Lys
 1 5 10 15
 Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg Asp Ala
 20 25 30
 Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser Pro Val
 35 40 45
 Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu Arg Pro
 50 55 60
 Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala
 65 70 75 80
 Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu His Thr
 85 90 95
 Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro Gln Pro
 100 105 110
 Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu His Arg
 115 120 125
 Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu Ala Ser
 130 135 140
 Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys Tyr Val
 145 150 155 160
 Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro Glu Ser Thr
 165 170 175

<210> 123

<211> 528

<212> DNA

<213> Artificial Sequence

<220>

<223> IL-29 C165X, truncated after N-terminal
 Methionine, Glycine, Proline, Valine, Proline,
 Threonine, and Serine

<221> CDS

<222> (1)...(528)

<221> variation

<222> (494)...(495)

<223> n = A, T, G, or C

<400> 123
 aag ccc acc aca act ggg aag ggc tgc cac att ggc agg ttc aaa tct 48
 Lys Pro Thr Thr Gly Lys Gly Cys His Ile Gly Arg Phe Lys Ser 15
 1 5 10
 ctg tca cca cag gag cta gcg agc ttc aag aag gcc agg gac gcc ttg 96
 Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg Asp Ala Leu 30
 20 25 30
 gaa gag tca ctc aag ctg aaa aac tgg agt tgc agc tct cct gtc ttc 144
 Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser Pro Val Phe 45
 35 40 45
 ccc ggg aat tgg gac ctg agg ctt ctc cag gtg agg gag cgc cct gtg 192
 Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu Arg Pro Val 60
 50 55 60
 gcc ttg gag gct gag ctg gcc ctg acg ctg aag gtc ctg gag gcc gct 240
 Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Ala 80
 65 70 75 80

gct ggc cca gcc ctg gag gac gtc cta gac cag ccc ctt cac acc ctg 288
 Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu His Thr Leu 95
 85

cac cac atc ctc tcc cag ctc cag gcc tgt atc cag cct cag ccc aca 336
 His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro Gln Pro Thr 110
 100 105

gca ggg ccc agg ccc cgg gcc cgc ctc cac cac tgg ctg cac cgg ctc 384
 Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu His Arg Leu 125
 115 120

cag gag gcc ccc aaa aag gag tcc gct gcc tgc ctg gag gca tct gtc 432
 Gln Glu Ala Pro Lys Lys Gln Ser Ala Gly Cys Leu Glu Ala Ser Val 140
 130 135

acc ttc aac ctc ttc cgc ctc ctc acg cga gac ctc aaa tat gtg gcc 480
 Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys Tyr Val Ala 160
 145 150 155

gat ggg aac ctg dnn ctg aga acg tca acc cac cct gag tcc acc tga 528
 Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro Glu Ser Thr * 175
 165 170

<210> 124

<211> 175

<212> PRT

<213> Artificial Sequence

<220>

<223> IL-29 C165X, truncated after N-terminal
 Methionine, Glycine, Proline, Valine, Proline,
 Threonine, and Serine

<221> VARIANT

<222> (165)...(165)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 124

Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly Arg Phe Lys Ser 15
 1 5 10
 Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg Asp Ala Leu 30
 20 25
 Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser Pro Val Phe 45
 35 40
 Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu Arg Pro Val 60
 50 55
 Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Ala 80
 65 70 75
 Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu His Thr Leu 95
 85 90
 His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro Gln Pro Thr 110
 100 105
 Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu His Arg Leu 125
 115 120
 Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu Ala Ser Val 140
 130 135
 Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys Tyr Val Ala 160
 145 150 155
 Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro Glu Ser Thr 175
 165 170

<210> 125
 <211> 552
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IL-29 Leu insert after N-terminal Met, C173X

<221> CDS
 <222> (1)...(552)

<221> variation
 <222> (6)...(6)
 <223> n = A, T, G, or C

<221> variation
 <222> (518)...(519)
 <223> n = A, T, G, or C

<400> 125
 atg ytn ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc 48
 Met Leu Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly 15
 1 5 10
 tgc cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc 96
 Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser 30
 20 25
 ttc aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac 144
 Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn 45
 35 40
 tgg agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt 192
 Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu 60
 50 55
 ctc cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg 240
 Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu 75 80
 65 70
 acg ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc 288
 Thr Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val 90 95
 85
 cta gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag 336
 Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln 110
 100 105
 gcc tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc 384
 Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg 125
 115 120
 ctc cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc 432
 Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser 140
 130 135
 gct ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc 480
 Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu 155 160
 145 150
 acg cga gac ctc aaa tat gtg gcc gat ggg aac ctg dnn ctg aga acg 528
 Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr 170 175
 165
 tca acc cac cct gag tcc acc tga 552

Ser Thr His Pro Glu Ser Thr *
180

<210> 126
<211> 183
<212> PRT
<213> Artificial Sequence

<220>
<223> IL-29 Leu insert after N-terminal Met, C173X

<221> VARIANT
<222> (173)...(173)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 126
Met Leu Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly
1 10 15
Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser
20 25 30
Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn
35 40 45
Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu
50 55 60
Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
65 70 75 80
Thr Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val
85 90 95
Leu Asp Gln Pro Leu His Thr Leu His Ile Leu Ser Gln Leu Gln
100 105 110
Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg
115 120 125
Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser
130 135 140
Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu
145 150 155 160
Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr
165 170 175
Ser Thr His Pro Glu Ser Thr
180

<210> 127
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-29 G2L C172X

<221> CDS
<222> (1)...(549)

<221> variation
<222> (6)...(6)
<223> n = A, T, G, or C

<221> variation
<222> (515)...(516)
<223> n = A, T, G, or C

<400> 127
atg ytn cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc tgc 48
Met Leu Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys

1 5 10 15
 cac att ggc agg ttc aaa tct ctg tca cca cag gag cta ggc agc ttc 96
 His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
 20 25 30
 aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg 144
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
 35 40 45
 agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc 192
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
 50 55 60
 cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg 240
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta 288
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95
 gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc 336
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
 100 105 110
 tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg gcc cgc ctc 384
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125
 cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct 432
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140
 ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg 480
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160
 cga gac ctc aaa tat gtg gcc gat ggg aac ctg dnn ctg aga acg tca 528
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser
 165 170 175
 acc cac cct gag tcc acc tga 549
 Thr His Pro Glu Ser Thr *
 180

<210> 128

<211> 182

<212> PRT

<213> Artificial Sequence

<220>

<223> IL-29 G2L C172X

<221> VARIANT

<222> (172)...(172)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 128

Met Leu Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys
 1 5 10 15
 His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
 20 25 30
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp

35 40 45
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
 50 55 60
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
 100 105 110
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser
 165 170 175
 Thr His Pro Glu Ser Thr
 180

<210> 129
 <211> 552
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IL-29 Ile insert after N-terminal Met, C173X

<221> CDS
 <222> (1)...(552)

<221> variation
 <222> (518)...(519)
 <223> n = A, T, G, or C

<400> 129
 atg ath ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc 48
 Met Ile Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly
 1 5 10 15
 tgc cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc 96
 Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser
 20 25 30
 ttc aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac 144
 Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn
 35 40 45
 tgg agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt 192
 Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu
 50 55 60
 ctc cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg 240
 Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
 65 70 75 80
 acg ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc 288
 Thr Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val
 85 90 95
 cta gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag 336
 Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln
 100 105 110

gcc tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc 384
 Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg
 115 120 125

ctc cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc 432
 Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser
 130 135 140

gct ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc 480
 Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu
 145 150 155 160

acg cga gac ctc aaa tat gtg gcc gat ggg aac ctg dnn ctg aga acg 528
 Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr
 165 170 175

tca-acc cac cct gag tcc acc tga 552
 Ser Thr His Pro Glu Ser Thr *
 180

<210> 130
 <211> 183
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IL-29 Ile insert after N-terminal Met, C173X

<221> VARIANT
 <222> (173)...(173)
 <223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 130
 Met Ile Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly
 1 5 10 15
 Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser
 20 25 30
 Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn
 35 40 45
 Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu
 50 55 60
 Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
 65 70 75 80
 Thr Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val
 85 90 95
 Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln
 100 105 110
 Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg
 115 120 125
 Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser
 130 135 140
 Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu
 145 150 155 160
 Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr
 165 170 175
 Ser Thr His Pro Glu Ser Thr
 180

<210> 131
 <211> 549
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IL-29 G2I C172X

<221> CDS
 <222> (1)...(549)

<221> variation
 <222> (515)...(516)
 <223> n = A, T, G, or C

<400> 131
 atg ath cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc tgc 48
 Met Ile Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys
 1 5 10 15
 cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc 96
 His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
 20 25 30
 aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg 144
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
 35 40 45
 agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc 192
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
 50 55 60
 cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg 240
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta 288
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95
 gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc 336
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
 100 105 110
 tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc 384
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125
 cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct 432
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140
 ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg 480
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160
 cga gac ctc aaa tat gtg gcc gat ggg aac ctg dnn ctg aga acg tca 528
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser
 165 170 175
 acc cac cct gag tcc acc tga 549
 Thr His Pro Glu Ser Thr *

<210> 132
 <211> 182
 <212> PRT
 <213> Artificial Sequence

<220>

<223> IL-29 G2I C172X

<221> VARIANT

<222> (172)...(172)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 132

```

Met Ile Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys
1      5      10      15
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
20      25      30
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
35      40      45
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
50      55      60
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
65      70      75      80
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
85      90      95
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
100      105      110
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
115      120      125
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
130      135      140
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145      150      155      160
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser
165      170      175
Thr His Pro Glu Ser Thr
180

```

<210> 133

<211> 531

<212> DNA

<213> Artificial Sequence

<220>

<223> IL-29 after N-terminal Met amino acid residues 2-7
deleted, C166X

<221> CDS

<222> (1)...(531)

<221> variation

<222> (497)...(498)

<223> n = A, T, G, or C

<400> 133

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atg aag ccc acc aca act ggg aag ggc tgc cac att ggc agg ttc aaa 48
Met Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly Arg Phe Lys
1      5      10      15
tct ctg tca cca cag gag cta gcg agc ttc aag aag gcc agg gac gcc 96
Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg Asp Ala
20      25      30
ttg gaa gag tca ctc aag ctg aaa aac tgg agt tgc agc tct cct gtc 144
Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser Pro Val
35      40      45
ttc ccc ggg aat tgg gac ctg agg ctt ctc cag gtg agg gag cgc cct 192
Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu Arg Pro

```

50

55

60

gtg gcc ttg gag gct gag ctg gcc ctg acg ctg aag gtc ctg gag gcc 240
 Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala
 65 70 75 80

gct gct ggc cca gcc ctg gag gac gtc cta gac cag ccc ctt cac acc 288
 Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu His Thr
 85 90 95

ctg cac cac atc ctc tcc cag ctc cag gcc tgt atc cag cct cag ccc 336
 Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro Gln Pro
 100 105 110

aca gca ggg ccc agg ccc cgg ggc cgc ctc cac cac tgg ctg cac cgg 384
 Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu His Arg
 115 120 125

ctc cag gag gcc ccc aaa aag gag tcc gct ggc tgc ctg gag gca tct 432
 Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu Ala Ser
 130 135 140

gtc acc ttc aac ctc ttc cgc ctc ctc acg cga gac ctc aaa tat gtg 480
 Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys Tyr Val
 145 150 155 160

gcc gat ggg aac ctg dnn ctg aga acg tca acc cac cct gag tcc acc 528
 Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro Glu Ser Thr
 165 170 175

tga 531
 *

<210> 134

<211> 176

<212> PRT

<213> Artificial Sequence

<220>

<223> IL-29 after N-terminal Met amino acid residues 2-7
 deleted, C166X

<221> VARIANT

<222> (166)...(166)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 134

Met Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly Arg Phe Lys
 1 5 10 15
 Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg Asp Ala
 20 25 30
 Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Pro Val
 35 40 45
 Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu Arg Pro
 50 55 60
 Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala
 65 70 75 80
 Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu His Thr
 85 90 95
 Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro Gln Pro
 100 105 110
 Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu His Arg
 115 120 125

Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu Ala Ser
 130 135 140
 Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys Tyr Val
 145 150 155 160
 Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro Glu Ser Thr
 165 170 175

<210> 135

<211> 558

<212> DNA

<213> Artificial Sequence

<220>

<223> IL-29 Glu, Ala, and Glu inserted after N-terminal
 Met, C175X

<221> CDS

<222> (1)... (558)

<221> variation

<222> (524)... (525)

<223> n = A, T, G, or C

<400> 135

atg gar gcn gar ggc cct gtc ccc act tcc aag ccc acc aca act ggg 48
 Met Glu Ala Glu Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly
 1 5 10 15

aag ggc tgc cac att ggc agg ttc aaa tct ctg tca cca cag gag cta 96
 Lys Gly Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu
 20 25 30

gcg agc ttc aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg 144
 Ala Ser Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu
 35 40 45

aaa aac tgg agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg 192
 Lys Asn Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu
 50 55 60

agg ctt ctc cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg 240
 Arg Leu Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu
 65 70 75 80

gcc ctg acg ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag 288
 Ala Leu Thr Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu
 85 90 95

gac gtc cta gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag 336
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
 100 105 110

ctc cag gcc tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg 384
 Leu Gln Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg
 115 120 125

ggc cgc ctc cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag 432
 Gly Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys
 130 135 140

gag tcc gct ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc 480
 Glu Ser Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
 145 150 155 160

ctc ctc acg cga gac ctc aaa tat gtg gcc gat ggg aac ctg dnn ctg 528
 Leu Leu Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu 175
 165 170

aga acg tca acc cac cct gag tcc acc tga 558
 Arg Thr Ser Thr His Pro Glu Ser Thr *
 180 185

<210> 136

<211> 185

<212> PRT

<213> Artificial Sequence

<220>

<223> IL-29 Glu, Ala, and Glu inserted after N-terminal
 Met, C175X

<221> VARIANT

<222> (175)...(175)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 136

Met Glu Ala Glu Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly
 1 5 10 15
 Lys Gly Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu
 20 25 30
 Ala Ser Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu
 35 40 45
 Lys Asn Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu
 50 55 60
 Arg Leu Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu
 65 70 75 80
 Ala Leu Thr Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu
 85 90 95
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
 100 105 110
 Leu Gln Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg
 115 120 125
 Gly Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys
 130 135 140
 Glu Ser Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
 145 150 155 160
 Leu Leu Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu
 165 170 175
 Arg Thr Ser Thr His Pro Glu Ser Thr
 180 185

<210> 137

<211> 528

<212> DNA

<213> Artificial Sequence

<220>

<223> Human IL-28A C2 mutant for expression in E. coli

<221> CDS

<222> (1)...(528)

<221> variation

<222> (146)...(147)

<223> n = A, T, G or C

<400> 137

atg gtt ccg gtt gct cgt ctg cac ggt gct ctg ccg gac gct cgt ggt 48
 Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly 15
 1 5 10

tgc cac atc gct cag ttc aaa tct ctg tct ccg cag gaa ctg cag gct 96
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala 30
 20 25

ttc aaa cgt gct aaa gac gct ctg gaa gaa tct ctg ctg ctg aaa gac 144
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp 45
 35 40

dnn cgt tgc cac tct cgt ctg ttc ccg cgt acc tgg gac ctg cgt cag 192
 Xaa Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln 60
 50 55

ctg cag gtt cgt gaa cgt ccg atg gct ctg gaa gct gaa ctg gct ctg 240
 Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu 80
 65 70 75

acc ctg aaa gtt ctg gaa gct acc gct gac acc gac ccg gct ctg gtt 288
 Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val 95
 85 90

gac gtt ctg gac cag ccg ctg cac acc ctg cac cac atc ctg tct cag 336
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln 110
 100 105

ttc cgt gct tgc atc cag ccg cag ccg acc gct ggt ccg cgt acc cgt 384
 Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg 125
 115 120

ggt cgt ctg cac cac tgg ctg tac cgt ctg cag gaa gct ccg aaa aaa 432
 Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys 140
 130 135

gaa tct ccg ggt tgc ctg gaa gct tct gtt acc ttc aac ctg ttc cgt 480
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg 160
 145 150 155

ctg ctg acc cgt gac ctg aac tgc gtt gct tct ggt gac ctg tgc gtt 528
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val 175
 165 170

<210> 138

<211> 176

<212> PRT

<213> Artificial Sequence

<220>

<223> Human IL-28A C2 mutant for expression in E. coli

<221> VARIANT

<222> (49)...(49)

<223> Xaa = Ser, Ala, Thr, Val or Asn

<400> 138

Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly 15
 1 5 10
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala 30
 20 25
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp 45
 35 40

Xaa Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
 50 55 60
 Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu
 65 70 75 80
 Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val
 85 90 95
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
 100 105 110
 Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
 115 120 125
 Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
 130 135 140
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
 145 150 155 160
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175

<210> 139
 <211> 528
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Human IL-28A C3 mutant for expression in E. coli

<221> CDS
 <222> (1)...(528)

<221> variation
 <222> (152)...(153)
 <223> n = A, T, G or C

<400> 139
 atg gtt ccg gtt gct cgt ctg cac ggt gct ctg ccg gac gct cgt ggt 48
 Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly
 1 5 10 15
 tgc cac atc gct cag ttc aaa tct ctg tct ccg cag gaa ctg cag gct 96
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
 20 25 30
 ttc aaa cgt gct aaa gac gct ctg gaa gaa tct ctg ctg ctg aaa gac 144
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
 35 40 45
 tgc cgt dnn cac tct cgt ctg ttc ccg cgt acc tgg gac ctg cgt cag 192
 Cys Arg Xaa His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
 50 55 60
 ctg cag gtt cgt gaa cgt ccg atg gct ctg gaa gct gaa ctg gct ctg 240
 Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu
 65 70 75 80
 acc ctg aaa gtt ctg gaa gct acc gct gac acc gac ccg gct ctg gtt 288
 Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val
 85 90 95
 gac gtt ctg gac cag ccg ctg cac acc ctg cac cac atc ctg tct cag 336
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
 100 105 110
 ttc cgt gct tgc atc cag ccg cag ccg acc gct ggt ccg cgt acc cgt 384
 Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
 115 120 125

ggt cgt ctg cac cac tgg ctg tac cgt ctg cag gaa gct ccg aaa aaa 432
 Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
 130 135 140
 gaa tct ccg ggt tgc ctg gaa gct tct gtt acc ttc aac ctg ttc cgt 480
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
 145 150 155 160
 ctg ctg acc cgt gac ctg aac tgc gtt gct tct ggt gac ctg tgc gtt 528
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175

<210> 140
 <211> 176
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human IL-28A C3 mutant for expression in E. coli
 <221> VARIANT
 <222> (51)...(51)
 <223> Xaa = Ser, Ala, Thr, Val or Asn

<400> 140
 Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly
 1 5 10 15
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
 20 25 30
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
 35 40 45
 Cys Arg Xaa His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
 50 55 60
 Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu
 65 70 75 80
 Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val
 85 90 95
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
 100 105 110
 Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
 115 120 125
 Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
 130 135 140
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
 145 150 155 160
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175

<210> 141
 <211> 528
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Human IL-28B C2 mutant for expression in E. coli
 <221> CDS
 <222> (1)...(528)
 <221> variation
 <222> 146, 147, 264

<223> n = A, T, G or C

<400> 141
 atg gtt ccg gtt gct cgt ctg cgt ggt gct ctg ccg gac gct cgt ggt 48
 Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly 15
 1 5 10
 tgc cac atc gct cag ttc aaa tct ctg tct ccg cag gaa ctg cag gct 96
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala 30
 20 25
 ttc aaa cgt gct aaa gac gct ctg gaa gaa tct ctg ctg ctg aaa gac 144
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp 45
 35 40
 dnn aaa tgc cgt tct cgt ctg ttc ccg cgt acc tgg gac ctg cgt cag 192
 Xaa Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln 60
 50 55
 ctg cag gtt cgt gaa cgt ccg gtt gct ctg gaa gct gaa ctg gct ctg 240
 Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu 80
 65 70 75
 acc ctg aaa gtt ctg gaa gct wsn gct gac acc gac ccg gct ctg ggt 288
 Thr Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly 95
 85 90
 gac gtt ctg gac cag ccg ctg cac acc ctg cac cac atc ctg tct cag 336
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln 110
 100 105
 ctg cgt gct tgc atc cag ccg cag ccg acc gct ggt ccg cgt acc cgt 384
 Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg 125
 115 120
 ggt cgt ctg cac cac tgg ctg yay cgt ctg cag gaa gct ccg aaa aaa 432
 Gly Arg Leu His His Trp Leu Xaa Arg Leu Gln Glu Ala Pro Lys Lys 140
 130 135
 gaa tct ccg ggt tgc ctg gaa gct tct gtt acc ttc aac ctg ttc cgt 480
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg 160
 145 150 155
 ctg ctg acc cgt gac ctg aac tgc gtt gct tct ggt gac ctg tgc gtt 528
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val 175
 165 170

<210> 142

<211> 176

<212> PRT

<213> Artificial Sequence

<220>

<223> Human IL-28B C2 mutant for expression in E. coli

<221> VARIANT

<222> (49)...(49)

<223> Xaa = Ser, Ala, Thr, Val or Asn

<221> VARIANT

<222> (88)...(88)

<223> Xaa = Thr or Ser

<221> VARIANT

<222> (136)...(136)

<223> Xaa = His or Tyr

<400> 142

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Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
1          5          10          15
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
20          25          30
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp
35          40          45
Xaa Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
50          55          60
Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
65          70          75          80
Thr Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly
85          90          95
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
100          105          110
Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
115          120          125
Gly Arg Leu His His Trp Leu Xaa Arg Leu Gln Glu Ala Pro Lys Lys
130          135          140
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
145          150          155          160
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
165          170          175

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<210> 143

<211> 528

<212> DNA

<213> Artificial Sequence

<220>

<223> Human IL-28B C3 mutant for expression in E. coli

<221> CDS

<222> (1)...(528)

<221> variation

<222> 152, 153, 264

<223> n = A, T, G or C

<400> 143

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atg gtt ccg gtt gct cgt ctg cgt ggt gct ctg ccg gac gct cgt ggt 48
Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
1          5          10          15
tgc cac atc gct cag ttc aaa tct ctg tct ccg cag gaa ctg cag gct 96
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
20          25          30
ttc aaa cgt gct aaa gac gct ctg gaa gaa tct ctg ctg ctg aaa gac 144
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
35          40          45
tgc aaa dnn cgt tct cgt ctg ttc ccg cgt acc tgg gac ctg cgt cag 192
Cys Lys Xaa Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
50          55          60
ctg cag gtt cgt gaa cgt ccg gtt gct ctg gaa gct gaa ctg gct ctg 240
Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
65          70          75          80

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acc ctg aaa gtt ctg gaa gct wsn gct gac acc gac ccg gct ctg ggt 288
 Thr Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly
 85 90 95

gac gtt ctg gac cag ccg ctg cac acc ctg cac cac atc ctg tct cag 336
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
 100 105 110

ctg cgt gct tgc atc cag ccg cag ccg acc gct ggt ccg cgt acc cgt 384
 Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
 115 120 125

ggt cgt ctg cac cac tgg ctg yay cgt ctg cag gaa gct ccg aaa aaa 432
 Gly Arg Leu His His Trp Leu Xaa Arg Leu Gln Glu Ala Pro Lys Lys
 130 135 140

gaa tct ccg ggt tgc ctg gaa gct tct gtt acc ttc aac ctg ttc cgt 480
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
 145 150 155 160

ctg ctg acc cgt gac ctg aac tgc gtt gct tct ggt gac ctg tgc gtt 528
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175

<210> 144

<211> 176

<212> PRT

<213> Artificial Sequence

<220>

<223> Human IL-28B C3 mutant for expression in E. coli

<221> VARIANT

<222> (51)...(51)

<223> Xaa = Ser, Ala, Thr, Val or Asn

<221> VARIANT

<222> (88)...(88)

<223> Xaa = Thr or Ser

<221> VARIANT

<222> (136)...(136)

<223> Xaa = His or Tyr

<400> 144

Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
 1 5 10 15
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
 20 25 30
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp
 35 40 45
 Cys Lys Xaa Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
 50 55 60
 Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
 65 70 75 80
 Thr Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly
 85 90 95
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
 100 105 110
 Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
 115 120 125
 Gly Arg Leu His His Trp Leu Xaa Arg Leu Gln Glu Ala Pro Lys Lys
 130 135 140

Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
 145 150 155 160
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175

<210> 145
 <211> 549
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Human IL-29 C1 mutant for expression in E. coli

<221> CDS
 <222> (1)....(549)

<221> variation
 <222> 33, 47, 48, 57
 <223> n = A, T, G or C

<400> 145
 atg ggt ccg gtt ccg acc tct aaa cca acc mcn act ggt aaa ggt dnn 48
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Xaa Thr Gly Lys Gly Xaa
 1 5 10 15
 cac atc grn cgt ttc aaa tct ctg tct ccg cag gaa ctg gct tct ttc 96
 His Ile Xaa Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
 20 25 30
 aaa aaa gct cgt gac gct ctg gaa gaa tct ctg aaa ctg aaa aac tgg 144
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
 35 40 45
 tct tgc tct tct ccg gtt ttc ccg ggt aac tgg gat ctg cgt ctg ctg 192
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
 50 55 60
 cag gtt cgt gaa cgt ccg gtt gct ctg gaa gct gaa ctg gct ctg acc 240
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 ctg aaa gtt ctg gaa gct gct gca ggt cct gct ctg gaa gat gtt ctg 288
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95
 gat cag ccg ctg cac act ctg cac cac atc ctg tct cag ctg cag gct 336
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
 100 105 110
 tgc att caa ccg caa ccg acc gct ggt ccg cgt ccg cgt ggt cgt ctg 384
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125
 cac cac tgg ctg cat cgt ctg cag gaa gct ccg aaa aaa gaa tct gct 432
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140
 ggt tgc ctg gaa gct tct gtt acc ttc aac ctg ttc cgt ctg ctg acc 480
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160
 cgt gat ctg aaa tac gtt gct gat ggt ray ctg tgc ctg cgt acc tct 528
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Xaa Leu Cys Leu Arg Thr Ser
 165 170 175

acc cat ccg gaa tct acc taa
 Thr His Pro Glu Ser Thr *
 180

<210> 146
 <211> 182
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human IL-29 C1 mutant for expression in E. coli

<221> VARIANT
 <222> (11)...(11)
 <223> Xaa = Thr or Pro

<221> VARIANT
 <222> (16)...(16)
 <223> Xaa = Ser, Ala, Thr, Val or Asn

<221> VARIANT
 <222> (19)...(19)
 <223> Xaa = Gly or Asp

<221> VARIANT
 <222> (170)...(170)
 <223> Xaa = Asn or Asp

<400> 146
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Xaa Thr Gly Lys Gly Xaa
 1 5 10 15
 His Ile Xaa Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
 20 25 30
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
 35 40 45
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
 50 55 60
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
 100 105 110
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Xaa Leu Cys Leu Arg Thr Ser
 165 170 175
 Thr His Pro Glu Ser Thr
 180

<210> 147
 <211> 549
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Human IL-29 C5 mutant for expression in E. coli

<221> CDS
 <222> (1)...(549)

<221> variation
 <222> 33, 57, 515, 516
 <223> n = A, T, G or C

<400> 147
 atg ggt ccg gtt ccg acc tct aaa cca acc mcn act ggt aaa ggt tgc 48
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Xaa Thr Gly Lys Gly Cys
 1 5 10 15

cac atc grn cgt ttc aaa tct ctg tct ccg cag gaa ctg gct tct ttc 96
 His Ile Xaa Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
 20 25 30

aaa aaa gct cgt gac gct ctg gaa gaa tct ctg aaa ctg aaa aac tgg 144
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
 35 40 45

tct tgc tct tct ccg gtt ttc ccg ggt aac tgg gat ctg cgt ctg ctg 192
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
 50 55 60

cag gtt cgt gaa cgt ccg gtt gct ctg gaa gct gaa ctg gct ctg acc 240
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80

ctg aaa gtt ctg gaa gct gct gca ggt cct gct ctg gaa gat gtt ctg 288
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95

gat cag ccg ctg cac act ctg cac cac atc ctg tct cag ctg cag gct 336
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
 100 105 110

tgc att caa ccg caa ccg acc gct ggt ccg cgt ccg cgt ggt cgt ctg 384
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125

cac cac tgg ctg cat cgt ctg cag gaa gct ccg aaa aaa gaa tct gct 432
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140

ggt tgc ctg gaa gct tct gtt acc ttc aac ctg ttc cgt ctg ctg acc 480
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160

cgt gat ctg aaa tac gtt gct gat ggt ray ctg dnn ctg cgt acc tct 528
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Xaa Leu Xaa Leu Arg Thr Ser
 165 170 175

acc cat ccg gaa tct acc taa 549
 Thr His Pro Glu Ser Thr *

<210> 148
 <211> 182
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human IL-29 C5 mutant for expression in E. coli

<221> VARIANT
 <222> (11)...(11)
 <223> Xaa = Thr or Pro

<221> VARIANT
 <222> (19)...(19)
 <223> Xaa = Gly or Asp

<221> VARIANT
 <222> (170)...(170)
 <223> Xaa = Asp or Asn

<221> VARIANT
 <222> (172)...(172)
 <223> Xaa = Ser, Ala, Thr, Val or Asn

<400> 148
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Xaa Thr Gly Lys Gly Cys
 1 5 10 15
 His Ile Xaa Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
 20 25 30
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
 35 40 45
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
 50 55 60
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
 100 105 110
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Xaa Leu Xaa Leu Arg Thr Ser
 165 170 175
 Thr His Pro Glu Ser Thr
 180

<210> 149
 <211> 531
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Human IL-29 d2/7 C5 mutant for expression in E.
 coli

<221> CDS
 <222> (1)...(531)

<221> variation
 <222> (497)...(498)
 <223> n = A, T, G or C

<400> 149
 atg aaa cca acc acc act ggt aaa ggt tgc cac atc ggt cgt ttc aaa 48
 Met Lys Pro Thr Thr Gly Lys Gly Cys His Ile Gly Arg Phe Lys
 1 5 10 15
 tct ctg tct ccg cag gaa ctg gct tct ttc aaa aaa gct cgt gac gct 96

```

Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg Asp Ala
      20      25      30
ctg gaa gaa tct ctg aaa ctg aaa aac tgg tct tgc tct tct ccg gtt 144
Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser Pro Val
      35      40      45
ttc ccg ggt aac tgg gat ctg cgt ctg ctg cag gtt cgt gaa cgt ccg 192
Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu Arg Pro
      50      55      60
gtt gct ctg gaa gct gaa ctg gct ctg acc ctg aaa gtt ctg gaa gct 240
Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala
      65      70      75      80
gct gca ggt cct gct ctg gaa gat gtt ctg gat cag ccg ctg cac act 288
Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu His Thr
      85      90      95
ctg cac cac atc ctg tct cag ctg cag gct tgc att caa ccg caa ccg 336
Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro Gln Pro
      100      105      110
acc gct ggt ccg cgt ccg cgt ggt cgt ctg cac cac tgg ctg cat cgt 384
Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu His Arg
      115      120      125
ctg cag gaa gct ccg aaa aaa gaa tct gct ggt tgc ctg gaa gct tct 432
Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu Ala Ser
      130      135      140
gtt acc ttc aac ctg ttc cgt ctg ctg acc cgt gat ctg aaa tac gtt 480
Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys Tyr Val
      145      150      155      160
gct gat ggt aac ctg dnn ctg cgt acc tct acc cat ccg gaa tct acc 528
Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro Glu Ser Thr
      165      170      175
taa
*
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<210> 150
 <211> 176
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human IL-29 d2/7 C5 mutant for expression in E.
 coli

<221> VARIANT
 <222> (166)...(166)
 <223> Xaa = Ser, Ala, Thr, Val or Asn

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<400> 150
Met Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly Arg Phe Lys
  1      5      10      15
Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg Asp Ala
      20      25      30
Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser Pro Val
      35      40      45
Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu Arg Pro
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50		55		60
Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala				
65		70		75
Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu His Thr				
	85		90	
Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro Gln Pro				
	100		105	
Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu His Arg				
	115		120	
Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu Ala Ser				
	130		135	
Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys Tyr Val				
145		150		155
Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro Glu Ser Thr				
	165		170	
				175

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